# WEST Search History

DATE: Thursday, June 08, 2006

| Hide? | Set Name | Query | Hit Count |
|:---:|:---|:---|---:|
| | | *DB=PGPB,USPT,JPAB,DWPI; PLUR=YES; OP=ADJ* | |
| ☐ | L6 | L5 and @pd > 20051011 | 3 |
| ☐ | L5 | L4 and (divergen$ or opposit$) | 36 |
| ☐ | L4 | L3 same enhancer | 46 |
| ☐ | L3 | L1 or L2 | 411 |
| ☐ | L2 | bi-direction$ near3 (promoter or regulator$ region or regulat$ element or regulat$ sequence) | 129 |
| ☐ | L1 | bidirection$ near3 (promoter or regulator$ region or regulat$ element or regulat$ sequence) | 321 |

END OF SEARCH HISTORY

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## Scientific and Technical Information Center
## SEARCH REQUEST FORM

Requester's Full Name: _Celine Qian_    Examiner # : _78710_  Date: _5/30/06_

Art Unit: _1636_    Phone Number: 2-_0777_    Serial Number: _10/075105_

Location (Bldg/Room#): _3.D24_ (Mailbox #): _2c70_   Results Format Preferred (circle): ⟨PAPER⟩ DISK

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: _Bi-directional dual promoter complex -_

Inventors (please provide full names): _Li, zhijian et al._

Earliest Priority Date: _2/13/2001_

### Search Topic:

*Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.*

*\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search SEQ ID NO: 1 (both commercial & interfera database). Thank you.

6/6/06
- wkm

RECEIVED MAY 30 2006 BIO/CHEM DIV.

/-736 na
18

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

GenCore version 5.1.9

Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June 5, 2006, 04:40:23 ; Search time 528 Seconds
(without alignments)
9718.892 Million cell updates/sec

Title:     US-10-075-105C-1
Perfect score:   736
Sequence:    1 ggatccagcgtgtcctcctcc...........ggagggaggacacgtcggatcc 736

Scoring table:   IDENTITY_NUC
             Gapop 10.0 , Gapext 1.0
Searched:    5244920 seqs, 348612423l residues

Total number of hits satisfying chosen parameters:   10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    N_Geneseq_8:*
          1: geneseqn1980s:*
          2: geneseqn1990s:*
          3: geneseqn2000o:*
          4: geneseqn2001as:*
          5: geneseqn2001bs:*
          6: geneseqn2002as:*
          7: geneseqn2002bs:*
          8: geneseqn2003as:*
          9: geneseqn2003bs:*
         10: geneseqn2003cs:*
         11: geneseqn2003ds:*
         12: geneseqn2004as:*
         13: geneseqn2004bs:*
         14: geneseqn2005s:*
         15: geneseqn2006s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

### SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 734.4 | 99.8 | 736 | 6 | ABS53103 | Abs53103 Transgene |
| 2 | 597.4 | 81.2 | 1360 | 6 | ABS53105 | Abs53105 Transgene |
| 3 | 554 | 75.1 | 661 | 1 | AAN81003 | Aan81003 Enhanced |
| 4 | 554 | 75.1 | 661 | 1 | AAN91710 | Aan91710 Enhanced |
| 5 | 554 | 75.3 | 2107 | 3 | AAD01017 | Aad01017 Expressio |
| 6 | 554 | 75.3 | 2122 | 3 | AAD01015 | Aad01015 Expressio |
| 7 | 554 | 75.3 | 2436 | 3 | AAD01018 | Aad01018 Expressio |
| 8 | 554 | 75.3 | 2767 | 15 | AEF22504 | Aef22504 RNAi tran |
| 9 | 554 | 75.3 | 3469 | 10 | AAZ51646 | Aaz51646 Bacillus |
| 10 | 554 | 75.3 | 3469 | 10 | AAD61794 | Aad61794 Bt.cry3Bb |
| 11 | 554 | 75.3 | 3469 | 15 | ABX95190 | Abx95190 B. thurin |
| 12 | 554 | 75.3 | 3469 | 15 | AEE66524 | Aee66524 Bt.cry3BB |
| 13 | 554 | 75.3 | 3754 | 10 | AAZ51642 | Aaz51642 Bacillus |
| 14 | 554 | 75.3 | 3754 | 10 | AAD61790 | Aad61790 Bt.cry3Bb |
| 15 | 554 | 75.3 | 3754 | 15 | ABX95186 | Abx95186 B. thurin |
| 16 | 554 | 75.3 | 3754 | 15 | AEE66516 | Aee66516 Bt.cry3Bb |
| 17 | 554 | 75.3 | 5170 | 12 | ADX98488 | Adx98488 B thuring |
| 18 | 554 | 75.3 | 5600 | 12 | ADX98490 | Adx98490 B thuring |

### ALIGNMENTS

RESULT 1
ID    ABS53103
AC    ABS53103 standard; DNA; 736 BP.
XX
PN    WO2002064804-A2.
XX
PD    22-AUG-2002.
XX
PF    13-FEB-2002; 2002WO-US004188.
XX
PR    13-FEB-2001; 2001US-0268358P.
XX
PA    (UYFL ) UNIV FLORIDA.
XX
PI    Li Z, Gray DJ;
XX
DR    WPI; 2002-627601/67.
XX
PT    New bi-directional promoter complex comprising a modified enhancer region
PT    including at least 2 enhancer sequences, and at least 2 core promoters,
PT    useful for enhancing, or improving transcriptional activity of transgenes.
XX
PS    Claim 9; Fig 2; 77pp; English.
XX
CC    29-NOV-2002 (first entry)
XX
DT    ABS53103;
XX
DE    Transgene expression related bidirectional dual promoter complex #1.
XX
KW    Bidirectional dual promoter complex; transcription; transgene;
KW    agronomic performance; transformation; ds.
XX
OS    Synthetic.
XX
FH    Key         Location/Qualifiers
FH
FT    misc_feature     1..736
FT                /tags= a
FT                /note= "The complement of this sequence is also claimed
FT                in claim 9 as SEQ ID number 2"

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 19 | 554 | 75.3 | 8012 | 2 | AAX57305 | Aax57305 Sugar bee |
| 20 | 554 | 75.3 | 8349 | 3 | AAA15565 | Aaa15565 pMON30464 |
| 21 | 554 | 75.3 | 8418 | 3 | AAX57309 | Aax57309 Sugar bee |
| 22 | 554 | 75.3 | 8798 | 2 | AAX57308 | Aax57308 Sugar bee |
| 23 | 553.2 | 75.2 | 7450 | 14 | ABA89733 | Aba89733 Novel tra |
| 24 | 551.4 | 74.9 | 1030 | 2 | AAV53707 | Aav53707 Nucleotid |
| 25 | 551.4 | 74.9 | 5796 | 4 | AAH25975 | Aah25975 Plant exp |
| 26 | 551.4 | 74.9 | 5897 | 2 | AAV63741 | Aav63741 Plasmid P |
| 27 | 551.4 | 74.9 | 3961 | 3 | AAD01285 | Aad01285 Rice tran |
| 28 | 551.4 | 74.9 | 10629 | 3 | AAD01286 | Aad01286 Rice tran |
| 29 | 550 | 74.7 | 9335 | 3 | AAV63734 | Aav63734 Plasmid P |
| 30 | 550 | 74.7 | 10249 | 3 | AAA15563 | Aaa15563 pMON31828 |
| 31 | 550 | 74.7 | 10312 | 3 | AAA15564 | Aaa15564 pMON31829 |
| 32 | 550 | 74.7 | 10339 | 3 | AAA15562 | Aaa15562 pMON31827 |
| 33 | 549.8 | 74.7 | 1030 | 15 | AEE47049 | Aee47049 Promoter |
| 34 | 549 | 74.6 | 3703 | 2 | AEE47049 | Aee47049 Chimeric |
| 35 | 548.4 | 74.5 | 1030 | 15 | AAQ76263 | Aaq76263 PNA lecti |
| 36 | 548.4 | 74.5 | 10160 | 2 | AAV63723 | Aav63723 Vector pl |
| 37 | 548.4 | 74.5 | 11784 | 2 | AAV63724 | Aav63724 Vector pl |
| 38 | 548.4 | 74.5 | 11991 | 2 | AAV63725 | Aav63725 Vector pl |
| 39 | 548 | 74.5 | 3563 | 15 | AEE47047 | Aee47047 Chimeric |
| 40 | 547 | 74.3 | 2881 | 15 | AEE47046 | Aee47046 Chimeric |
| 41 | 547 | 74.3 | 3773 | 15 | AEE47048 | Aee47048 Chimeric |
| 42 | 545.2 | 74.1 | 612 | 14 | AEB45238 | Aeb45238 35S promo |
| 43 | 543.6 | 73.9 | 4119 | 3 | AAZ51641 | Aaz51641 Bacillus |
| 44 | 543.6 | 73.9 | 4119 | 10 | AAD61789 | Aad61789 Bt.cry3Bb |
| 45 | 543.6 | 73.9 | 4119 | 10 | ABX95185 | Abx95185 B. thurin |

```
CC   The invention describes a bi-directional promoter complex comprising a
CC   modified enhancer region that includes at least 2 enhancer sequences, and
CC   at least 2 core promoters. The core promoters are on either side of the
CC   modified enhancer region in a divergent orientation. The bi-directional
CC   promoter complex is useful for enhancing transcriptional activity of
CC   transgenes to improve agronomic performance used in genetic
CC   transformation with plants. Vectors that include the bi-directional
CC   promoter complex may be used to express foreign genes in mammalian cells
CC   and in plant cells including dicots and monocots. This sequence
CC   represents a bidirectional dual promoter complex useful for enhancing
CC   transcriptional activity of transgenes
XX
SQ   Sequence 736 BP; 222 A; 176 C; 175 G; 163 T; 0 U; 0 Other;

Query Match         99.8%;  Score 734.4;  DB 6;  Length 736;
Best Local Similarity   99.9%;  Pred. No. 8.1e-232;
Matches  735;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy          1 GGATCCAGCCGTGTCCTCTCCAAATGAAATGAACTTCCTTATATAGGAAGGGTCTTGCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGATCCAGCCGTGTCCTCTCCAAATGAAATGAACTTCCTTATATAGGAAGGGTCTTGCG 60

Qy         61 AAGGAGTAGTGGGATTGTGCGTCATCCCTTACGTGCGTGAGATACTGCGAGAAGCTTCTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGGAGTAGTGGGATTGTGCGTCATCCCTTACGTGCGTGAGATACTGCGAGAAGCTTCTGC 120

Qy        121 AGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 180

Qy        181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGCACCTACAAATGCCATCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGCACCTACAAATGCCATCAT 240

Qy        241 TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300

Qy        301 CCCCCACCCCACGGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCCCCACCCCACGGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 360

Qy        361 GTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGATTGATGTGATTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTC 420

Qy        421 GGATTCAATTGCCCAGCTATCGTGCTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGATTCAATTGCCCAGCTATCGTGCTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGC 480

Qy        481 ACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGAC 540

Qy        541 AGTGGTCCCAAAGATGGACCCCCACCCCACGGAGGAGCATCGTGGAAAAAGACGTTCCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGTGGTCCCAAAGATGGACCCCCACCCCACGGAGGAGCATCGTGGAAAAAGACGTTCCA 600

Qy        601 ACCACGTCTTCAAAGCAAGTGGATTGGATTGGATGTATATCTCCACTGACGTAAGGGATGACGGA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACCACGTCTTCAAAGCAAGTGGATTGGATTGGATGTATATCTCCACTGACGTAAGGGATGACGGA 660

Qy        661 CAATCCCAACTATCCTTCGCAAGACCCTTCCTCCTATATTAAGGAAGTTCATTTCATTTGGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAATCCCAACTATCCTTCGCAAGACCCTTCCTCCTATATTAAGGAAGTTCATTTCATTTGGAG 720

Qy        721 AGGACACGCTGGATCC 736
              ||||||||||||||||
Db        721 AGGACACGCTGGATCC 736

RESULT 2
ABS53105
```

```
ID   ABS53105 standard; DNA; 1360 BP.
XX
AC   ABS53105;
XX
DT   29-NOV-2002 (first entry)
XX
DE   Transgene expression related bidirectional dual promoter complex #2.
XX
KW   Bidirectional dual promoter complex; transcription; transgene;
KW   agronomic performance; transformation; ds.
XX
OS   Synthetic.
XX
FH   Key                 Location/Qualifiers
FH
FT   misc_feature        1..1360
FT                       /*tag= a
FT                       /note= "the complement of this sequence is also claimed
FT                       in claim 10 as SEQ ID number 4"
XX
PN   WO20264804-A2.
XX
PD   22-AUG-2002.
XX
PF   13-FEB-2002; 2002WO-US004188.
XX
PR   13-FEB-2001; 2001US-0268358P.
XX
PA   (UYFL ) UNIV FLORIDA.
XX
PI   Li Z, Gray DJ;
XX
DR   WPI; 2002-627601/67.
XX
PT   New bi-directional promoter complex comprising a modified enhancer region
PT   including at least 2 enhancer sequences, and at least 2 core promoters,
PT   useful for enhancing or improving transcriptional activity of transgenes.
XX
PS   Claim 10; Fig 4; 77pp; English.
XX
CC   The invention describes a bi-directional promoter complex comprising a
CC   modified enhancer region that includes at least 2 enhancer sequences, and
CC   at least 2 core promoters. The core promoters are on either side of the
CC   modified enhancer region in a divergent orientation. The bi-directional
CC   promoter complex is useful for enhancing transcriptional activity of
CC   transgenes to improve agronomic performance used in genetic
CC   transformation with plants. Vectors that include the bi-directional
CC   promoter complex may be used to express foreign genes in mammalian cells
CC   and in plant cells including dicots and monocots. This sequence
CC   represents a bidirectional dual promoter complex useful for enhancing
CC   transcriptional activity of transgenes
XX
SQ   Sequence 1360 BP; 353 A; 319 C; 317 G; 371 T; 0 U; 0 Other;

Query Match         81.2%;  Score 597.4;  DB 6;  Length 1360;
Best Local Similarity   99.8%;  Pred. No. 2.2e-186;
Matches  598;  Conservative   1;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTC 168
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        762 ATAAGCTTCTGCAGTGAGACTTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTC 821

Qy        169 CATTGCCCAGCTATCCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGCACCTAC 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        822 CATTGCCCAGCTATCCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTGGCACCTAC 881

Qy        229 AAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGCACGTGGT 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        882 AAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGCACGTGGT 941

Qy        289 CCCAAAGATGAGCCCCCACCCCACGGAGGAGCATCGTGGAAAAAGACGTTCCAACCACG 348
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        942 CCCAAAGATGAGCCCCCACCCCACGGAGGAGCATCGTGGAAAAAGACGTTCCAACCACG 1001
```

RESULT 3

```
ID   AAN81003  standard; DNA; 661 BP.
XX
AC   AAN81003;
XX
DT   03-NOV-1990  (first entry)
XX
DE   Enhanced CaMV35S promoter used in pMON893 B.thuringiensis toxin prodn.
XX
KW   Bacillus thuringiensis var. tenebrionis toxin gene; enhanced promoter;
KW   CaMV35S; pMON893; Coleopteran insects; transformed plants; ss.
OS   chimeric gene; ss.
XX
FH   Bacillus thuringiensis.
XX
FH   Key                 Location/Qualifiers
FT
FT   misc_feature        27..279
FT                       /*tag= a
FT                       /number= 1
FT                       /note="duplicated enhancer"
FT   misc_feature        289..541
FT                       /*tag= b
FT                       /number= 2
FT                       /note="duplicated enhancer"
XX
EP289479-A.
PN
PD   02-NOV-1988.
XX
PF   26-APR-1988;  88EP-00870070.
XX
PR   29-APR-1987;  87US-0004081.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Fischhoff DA,  Fuchs RL,  Mcpherson SA,  Lavrik PB,  Perlak FJ;
XX
DR   WPI; 1988-309416/44.
XX
PT   Genetically transformed plants with toxicity to Coleopteran insects -
PT   obtd. using chimeric gene contg. sequence encoding toxin protein of
PT   Bacillus thuringiensis.
XX
PS   Disclosure; Page 7; 52pp; English.
XX
CC   A fragment of the CaMV35S promoter (-343 to +9), previously constructed
CC   by Odell et al. (1985) Nature 313;810-812, is necessary for maximal
```

```
CC   expression of the promoter. It was exiced as a ClaI-HindIII fragment,
CC   made blunt ended with DNA pol I and inserted into the HincII site of
CC   pUC18. The upstream region of the 35S promoter was exiced from this
CC   plasmid as a HindIII-EcoRV fragment (-343 to -90) and inserted into the
CC   ssame plasmid between the HindIII and PstI sites. The enhanced promoter
CC   thus contains a duplication of sequences -343 to -90. See also AAN81000-
CC   N81003
XX
SQ   Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;
```

Query Match   75.3%; Score 554; DB 1; Length 661;
Best Local Similarity  94.5%; Pred. No. 3.4e-172;
Matches 586; Conservative  0; Mismatches  30; Indels  4; Gaps  1;

```
Qy   349 TCTTCAAAGCAAGTGGATTGAATGCAGTGAGTGAGACTTTTCAACAAAGGGTAATATCG 408
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1002 TCTTCAAAGCAAGTGGATTGAATGCAGTGAGTGAGACTTTTCAACAAAGGGTAATATCG 1061

Qy   409 GGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTCATTGCCCAGCTATCGGA 468
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1062 GGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTCATTGCCCAGCTATCGGA 1121

Qy   469 AAGGAAGTGGCACCTACAAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGAT 528
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1122 AAGGAAGTGGCACCTACAAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGAT 1181

Qy   529 GCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACCCACGAGGAGCATCGTGGAAAAA 588
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1182 GCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCACCCACGAGGAGCATCGTGGAAAAA 1241

Qy   589 GAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 648
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1242 GAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTA 1301

Qy   649 AGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTC 707
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1302 AGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTC 1360
```

RESULT 4

```
ID   AAN91710  standard; DNA; 661 BP.
XX
AC   AAN91710;
XX
DT   25-MAR-2003  (revised)
DT   12-MAR-1990  (first entry)
XX
DE   Enhanced CaMV35S promoter used in plasmid pMON893.
XX
KW   CaMV35S promoter; Bacillus thuringiensis; toxin protein; insecticide;
KW   plasmid pMON893.
XX
```

Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;

```
Qy   116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    20 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 79

Qy   176 CAGCTATCTGTCACTTCATCAAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCC 235
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    80 CAGCTATCTGTCACTTTATTGTGGAAGATAGTGGAAAAGGAAGGTGGCTCCTTACAAAATGCC 139

Qy   236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACACGTGGTCCCAAAG 295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   140 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 199

Qy   296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 259

Qy   356 AGCAAGTGGATTGATGTGAT---TCGACTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
         ||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db   260 AGCAAGTGGATTGATGTGATATCTCCACTGAGACTTTTCAACAAAGGGTAATATCGGA 319

Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCATCAAAAAGGACAGTAGAAAAG 471
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   320 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGGAAGATAGTGGAAAAG 379

Qy   472 GAAGGTGGCACCTACAATCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   380 GAAGGTGGCTCCTTACAATCCATCATTGCGATAAAGGAAAGGCCATGTTCAAGATGCC 439

Qy   532 TCTGCCGACAGTGGTCCCAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGA 591
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   440 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGGA 499

Qy   592 GAAGCGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 651
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   500 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 559

Qy   652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTT 711
         ||||||||||||||||||||||||||||||||||||
Db   560 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTT 619

Qy   712 CATTTGGAGAGGACACGCTG 731
         ||||||||||||||||||||
Db   620 CATTTGGAGAGGACACGCTG 639
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OS    Cauliflower mosaic virus.
XX
FH    Key             Location/Qualifiers
FT    misc_feature    27..279
FT                    /*tag= a
FT                    /note= "duplicated enhancer sequence"
FT    misc_feature    289..541
FT                    /*tag= b
FT                    /note= "duplicated enhancer sequence"
XX
PN    EP339009-A.
XX
PD    25-OCT-1989.
XX
PF    14-APR-1989;  89EP-00870047.
XX
PR    11-APR-1988;  88US-00179709.
XX
PA    (MONS ) MONSANTO CO.
XX
PI    Fuchs RL, Kishore GM, Macintosh SC;
XX
DR    WPI; 1989-311431/43.
XX
PT    Toxin protein of Bacillus thuringiensis bacteria - improved in efficacy
PT    using a potentiating amt. of a trypsin inhibitor.
XX
PS    Disclosure; Fig 14; 56pp; English.
XX
CC    A fragment of the CamV35S promoter (-343 to +9) in pUC13 was excised as a
CC    ClaI-HindIII fragment and blunt-ended. This was inserted into the HincII
CC    site of pUC18. The upstream region of the 35S promoter was excised as a
CC    HindIII-EcoRV fragment (extending from -343 to -90) and inserted into the
CC    same plasmid between the HindIII and PstI sites. The enhanced promoter
CC    thus contains a duplication of sequences between -343 ans -90. The
CC    promoter is used in plasmid pMON893 to express Bacillus thuringiensis
CC    toxin with a potentiating amt. of a trypsin inhibitor. This is useful as
CC    an insecticide. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ    Sequence 661 BP; 194 A; 160 C; 157 G; 150 T; 0 U; 0 Other;

Query Match     75.3%;  Score 554; DB 1; Length 661;
Best Local Similarity   94.5%;  Pred. No. 3.4e-172;
Matches  586;  Conservative    0;  Mismatches   30;  Indels    4;  Gaps    1;

Qy    116 TCTGCCAGTGAGGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCAATGCC 175
          |||||||||||||||| ||||||||||||||||||| |||||||||||||||||||||||||
Db     20 TCCGATGTGAGGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCAATGCC 79

Qy    176 CAGCTATCTGTCACTTCATCAAAGACAGTAGAAAAGGACGAGGTGGCCACCTACAAATGCC 235
          |||||||||| || ||||||||| ||| |||||||| |||||||||| |||| |||||||||
Db     80 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGACGAGGTGGCTTCCTACAAATGCC 139

Qy    236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCGCCAGACGTGGTCCCAAAG 295
          ||||||||||||||||||| ||||| ||||||||||||||||| |||||||||||||||
Db    140 ATCATTGCGATAAAGGAAAGGCCCATGCCTCGCCAGACGTGGTCCCAAAG 199

Qy    296 ATGGACCCCACCCCACGGAGGAGCATCGTTGAAAAAGAAGACGTTCAACCACGTCTTCAA 355
          |||||||||||||||||||||||||||||| ||| |||||||||| ||||||||||||||
Db    200 ATGGACCCCACCCCACGGAGGAGCATCGTTGAAAAAGAAGACGTTCAACCACGTCTTCAA 259

Qy    356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGGACTTTTCAACAAAGGGTAATATCGGGA 411
          |||||||||||||||||||||   |    ||||||||||||||||||||||||||||||||
Db    260 AGCAAGTGGATTGATGTGGTCCGATGGTGAGGACTTTTCAACAAAGGGTAATATCCGGA 319

Qy    412 AACCTCCTCGGATTCCAATTGCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
          |||||||||||||||| ||| || ||||||||||||||||| | | |||||||||| |||||
Db    320 AACCTCCCTCGGATTCCAATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTAGTGAAAAG 379

Qy    472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
          |||||||||||||||||||||||||||||||||||| |||||||||| |||||||||||
Db    380 GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGAAGGCATCGTTGAAGATGCC 439

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Qy    532 TCTGCCGACAGTGTCCAAAGATGGACCCCACCCCACCCGAGGAGCATCGTTGGAAAAAGAA 591
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    440 TCTGCCGACAGTGTCCAAAGATGGACCCCACCCCACCCGAGGAGCATCGTTGGAAAAAGAA 499

Qy    592 GACGTTCCAACCAGTGTCTTCAAAGCAAGTGGATTGGATTGGATATCTCCACTGACGTAAGG 651
          |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db    500 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGGATTGGATATCTCCACTGACGTAAGG 559

Qy    652 GATGACGGACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 GATGACGGACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 619

Qy    712 CATTTGGAGGACGACGCGCTG 731
          |||||||||||||||||||||
Db    620 CATTTGGAGGACGACGCGCTG 639

---

RESULT 5
AAD01017
ID    AAD01017 standard; DNA; 2107 BP.
XX
AC    AAD01017;
XX
DT    21-SEP-2000  (first entry)
XX
DE    Expression cassette-4 comprising modified E. coli P2A phnO coding gene.
XX
KW    Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
KW    acyltransferase; transacylase; recombinant plant; expression cassette;
KW    corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;
KW    CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene;
KW    self-fertilisation; hetero-fertilisation; ds.
XX
OS    Escherichia coli.
OS    Synthetic.
XX
FH    Key             Location/Qualifiers
FT    promoter        26..590
FT                    /*tag= a
FT                    /note= "Plant functional heterologous promoter"
FT    5'UTR           615..685
FT                    /*tag= b
FT                    /note= "Enhances expression of the phnO gene"
FT    intron          699..1148
FT                    /*tag= c
FT                    /note= "Enhances expression of the phnO gene"
FT    transit_peptide 1149..1426
FT                    /*tag= d
FT                    /note= "Targets the protein to an intracellular
FT                    organelle, like chloroplast"
FT    CDS             1427..1861
FT                    /*tag= e
FT                    /product= "Escherichia coli modified P2A AMPA
FT                    acyltransferase (AAT) enzyme"
FT                    /function= "Transfers acyl group from an acylcarrier
FT                    (CoA) to the free amino group of aminomethylphosphonate"
FT    terminator      1869..2102
FT                    /*tag= f
XX
PN    WO200029596-A1.
XX
PD    25-MAY-2000.
XX
PF    16-NOV-1999;  99WO-US027152.
XX
PR    17-NOV-1998;  98US-01087763P.
XX
PA    (MONS ) MONSANTO CO.
XX
PI    Barry GF;
XX
DR    WPI; 2000-387806/33.
DR    P-PSDB; AAY71251.

XX
PT  Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
PT  cotton, canola and rice plants involves transforming plants with
PT  phosphonate metabolizing genes encoding acyltransferase enzyme.
XX
PS  Disclosure; Page 170-172; 179pp; English.
XX

The patent discloses a method for selectively enhancing the phosphonate
herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
and rice plants, by transforming the plants with an expression cassette.
It comprises of a structural DNA sequence, that encodes an aminomethyl
phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of
N-acylation of AMPA. This sequence has an amino terminal chloroplast
transit peptide (CTP), that targets AAT to the chloroplast. Co-expression
of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,
along with AAT provides the transformed plants with higher resistance to
phosphonate herbicides. This method is useful for enhancing phosphonate
herbicides such as glyphosate and AMPA tolerance, in recombinant plants
and to prevent self-fertilisation and enhance hetero-fertilisation. The
present DNA sequence is the expression cassette-4, comprising a plant
operable promoter and 5' sequences like, 5' untranslated region (UTR) and
intron, linked to modified E. coli phnO coding region encoding P2A AMPA
acyltransferase (AAT) enzyme and plant operable termination sequences

SQ  Sequence 2107 BP; 497 A; 531 C; 551 G; 528 T; 0 U; 0 Other;

Query Match          75.3%;  Score 554;  DB 3;  Length 2107;
Best Local Similarity 94.5%;  Pred. No. 6e-172;
Matches 586;  Conservative 0;  Mismatches 30;  Indels 4;  Gaps 1;

```
Qy    116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAA                     175
          |||| |||||||||||||||||||||||||| |||||||
Db     28 TCCGARGTGAGACTTTTCAACAAAGGGTAATATCCGGGAAACCCCTCCGGATTCCATTGCC 87

Qy    176 CAGCTATCTTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAGGTGGCACCTACAAATGCC 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 CAGCTATCTTGTCACTTTATTGTGAAGATAGTGGAAAAGGAGGTGGCACCTACAAATGCC  147

Qy    236 ATCATTCGGATAAAAGGAAAGGCTATCGTTCAAGATGCGCTTCGCCACAGTGGTCCCAAAG 295
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 ATCATTCGGATAAAAGGAAAGGCCATCGTTGAAGATGCCTCTCGCCACGTGGTCCCAAAG  207

Qy    296 ATGGACCCCCACCCAGCAGCGAGCATGCTGGAAAAAGAAGAGACCTTCCAACCACGGTCTT 355
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 ATGGACCCCCACCCAGCGGCATGCGTGGAAAAAGAGAGGACGTTCCAACCACCGGTCTTCA 267

Qy    356 ACCAAGTGGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
          |||||||||||| || ||||    ||||||||||||||||||||||||||||||||||||
Db    268 AGGAAGTGGGATTGATGTGATGGTCCGGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy    412 AACCCCTCCGGATTCCATTGCCCAGCTACTCTATCACTTCATCAAAAGGACAGTAGAAAAA 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCCCTCCGGATTCCATTGCCCAGCTACTCTATCACTTCATCAAAAGGACAGTAGAAAAAG 387

Qy    472 GAAGGTGGCACCTACAAATGCCATCATTCCGGATAAAAGCAAAGGCTATCGTTCAAGATGCC 531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    388 GAAGGTGGCTCCTACAAATGCCATCATTGCGGATAAAAGGCATCGTTGAAGATGCC      447

Qy    532 TCTGCCGCACAGTGGTCCAAAGATGACCCCCACCCACAGGAGCGAGCATGCTGGAAAAAGA 591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 TCTCGCCGCACAGTGGTCCCAAAGATGACCCCCACGCGAGCGAGCATGCTGGAAAAAGA   507

Qy    592 GACGTTCCAACCACCGGTCTTCAAGGCAAGCAAGGTGGATTGATGTGATGGTCCACTGAGG 651
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 GACGTTCCAACCACCGGTCTTCAAACGCAAGGTGGATTGATGTGATTATCTCCACTGACGTAAGG 567

Qy    652 GATGAGCGCAATCCCACTATCCTTCGCAAGACCCTTCCTTATAATPAGGAACTTCATTT   711
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GATGAGCGACAATCCCACTATCCTTCGCAAGACCCTTCCTTATAATPAGGAACTTCATTT  627

Qy    712 CATTTGGAGGAGGACAGCCTG                                         731
          |||||||||||||||||||||
Db    628 CATTTGGAGGAGGACAGCCTG                                          647
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RESULT 6
XX
AC  AAD01015
XX
ID  AAD01015 standard; DNA; 2122 BP.
XX
AC  AAD01015;
XX
DT  21-SEP-2000  (first entry)
XX
DE  Expression cassette-2 comprising modified E. coli P2A phnO coding gene.
XX
KW  Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
KW  acyltransferase; transacylase; recombinant plant; expression cassette;
KW  corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;
KW  CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene;
KW  self-fertilisation; hetero-fertilisation; ds.
XX
OS  Escherichia coli.
OS  Synthetic.
XX

Key                Location/Qualifiers
FH
FT  promoter        6..620
FT                  /tag= a
FT                  /note= "plant functional heterologous promoter"
FT  5'UTR           645..715
FT                  /tag= b
FT                  /note= "Enhances expression of the phnO gene"
FT  intron          729..1178
FT                  /tag= c
FT                  /note= "Enhances expression of the phnO gene"
FT  transit_peptide 1179..1406
FT                  /tag= d
FT                  /note= "Targets the protein to an intracellular
FT                  organelle, like chloroplast"
FT  CDS             1407..1841
FT                  /tag= e
FT                  /product= "Escherichia coli modified P2A AMPA
FT                  acyltransferase (AAT) enzyme"
FT                  /function= "Transfers acyl group from an acylcarrier
FT                  (CoA) to the free amino group of aminomethylphosphonate"
FT  terminator      1849..2082
FT                  /tag= f

XX
PN  WO200029596-A1.
XX
PD  25-MAY-2000.
XX
PF  16-NOV-1999;  99WO-US027152.
XX
PR  17-NOV-1998;  98US-0108763P.
XX
PA  (MONS ) MONSANTO CO.
XX
PI  Barry GP;
XX
DR  WPI; 2000-387806/33.
DR  P-PSDB; AAY712251.
XX
PS  Disclosure; Page 164-166; 179pp; English.
XX
PT  Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
PT  cotton, canola and rice plants involves transforming plants with
PT  phosphonate metabolizing genes encoding acyltransferase enzyme.
XX

CC  The patent discloses a method for selectively enhancing the phosphonate
CC  herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
CC  and rice plants, by transforming the plants with an expression cassette.
CC  It comprises of a structural DNA sequence, that encodes an aminomethyl
CC  phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of
CC  N-acylation of AMPA. This sequence has an amino terminal chloroplast
CC  transit peptide (CTP), that targets AAT to the chloroplast. Co-expression
CC  of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,

CC  along with AAT provides the transformed plants with higher resistance to
CC  phosphonate herbicides. This method is useful for enhancing phosphonate
CC  herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC  and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC  present DNA sequence is the expression cassette-2, comprising a plant
CC  operable promoter and 5' sequences like, 5'-untranslated region (UTR) and
CC  intron, linked to modified E. coli phnO coding region encoding P2A AMPA
CC  acyltransferase (AAT) enzyme and plant operable termination sequences
XX
SQ  Sequence 2122 BP; 495 A; 537 C; 561 G; 529 T; 0 U; 0 Other;

Query Match             75.3%;  Score 554; DB 3; Length 2122;
Best Local Similarity   94.5%;  Pred. No. 6e-172;
Matches  586;  Conservative   0;  Mismatches  30;  Indels    4;  Gaps    1;

Qy     116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCCGGGAAACCTCCTCCGGATTCCATTGCC 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8 TCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGGAAACCTCCTCCGGATTCCATTGCC 67

Qy     176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAAAGGTGGCGCCTACAAATGCC 235
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 CAGCTATCTGTCACTTTATTGTAGAGATAGGTGAAAAAGGAAAAGGTGGCTCCTACAAATGCC 127

Qy     236 ATCATTGGCGATAAAAGGAAAAGGCTATCGTTCAACGATGCCTCTGCCGACACTAGCTCCAAAG 295
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 ATCATTGGCGATAAAAGGAAAAGGCCATCGTTGAAGGATGCCTCTGCCGACACAGTGCTCCAAAG 187

Qy     296 ATGGACCCCCACCCCACCGAGGGAGGCATCGTGGAAAAAGGAAAAGGGCTATCGTTCAACGAG 355
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 ATGGACCCCCACCCCACCGAGGGAGGCATCGTGGAAAAAGGAAAAGGGCTATCGTTCAACGAG 247

Qy     356 AGCAAGTGGATTGATGTGAT----TGCAGTCAGAGACTTTTCAACAAAGGGTAATATCCGGGA 411
           ||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||||||
Db     248 AGCAAGTGGATTGATGTGATCGTCCGATGTCAGAGACTTTTCAACAAAGGGTAATATCCGGGA 307

Qy     412 AACCTCCTCGGATTCCATTGCCCCAGCTATCGTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 AACCTCCTCGGATTCCATTGCCCCAGCTATCGTGTCACTTTATTGTGAAGATAGTGTAGAAAAG 367

Qy     472 GAAGGTGGCGACTACAAATGCCATCATTGCGATAAAAGGAAAAGGCTATCGTTCAACGATGCC 531
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 GAAGGTGGCTCTTACAAATGCCATCATTGCGATAAAAGGAAAAGGCCATCGTTGAAGAATGCC 427

Qy     532 TCTGCCGACACAGTGGTCGTTCCCAAAGATGACCCCCACCCCACCGAGGGAGGCATCGTGGAAAAAGA 591
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     428 TCTGCCGACACAGTGGTCGTCCCCAAGATGACCCCCACCCCACCGAGGGAGGCATCGTGGAAAAAGA 487

Qy     592 GACGTTCCAACCACGCTTCTTCAAAGCAAGTGGATTGATGTGATATATCCACTGACCTAAGG 651
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     488 GACGTTCCAACCACGCTTCTTCAAGCAAGTGGATTGATGTGTATATCCACTGACCTGAAGG 547

Qy     652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTTCTATATAAGGAAGTTCATTT 711
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     548 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTTCTATATAAGGAAGTTCATTT 607

Qy     712 CATTTGGAGGAGGACGGCGTG 731
           |||||||||||||||||||||
Db     608 CATTTGGAGGAGGACGGCGTG 627

RESULT 7
ID  AAD01018
AC  AAD01018;
XX
DT  21-SEP-2000  (first entry)
XX
DE  Expression cassette-5 comprising modified E. coli P2A phnO coding gene.
XX
KW  Phosphonate herbicide tolerance; aminomethyl phosphonic acid; AMPA; AAT;
KW  acyltransferase; transacylase; recombinant plant; expression cassette;
KW  corn; tobacco; wheat; cotton; canola; rice; chloroplast transit peptide;
KW  CTP; glyphosate oxidase; GOX; glyphosate oxidoreductase; phnO gene;
KW  self-fertilisation; hetero-fertilisation; de.
XX
OS  Bacterichia coli.
OS  Synthetic.
XX
KW  Key             Location/Qualifiers
FH
FT  promoter        26..640
FT                  /note= a
FT                  /note= "Plant functional heterologous promoter"
FT  intron          670..1473
FT                  /*tag= b
FT                  /note= "Enhances expression of the phnO gene"
FT  transit_peptide 1498..1725
FT                  /*tag= c
FT                  /note= "Targets the protein to an intracellular
FT                  organelle, like chloroplast"
FT  CDS             1726..2160
FT                  /*tag= d
FT                  /product= "Escherichia coli modified P2A AMPA
FT                  acyltransferase (AAT) enzyme"
FT                  /function= "Transfers acyl group from an acylcarrier
FT                  (CoA) to the free amino group of aminomethylphosphonate"
FT  terminator      2172..2427
FT                  /*tag= e
XX
PN  WO200029596-A1.
XX
PD  25-MAY-2000.
XX
PF  16-NOV-1999;  99WO-US0271152.
XX
PR  17-NOV-1998;  98US-0108763P.
XX
PA  (MONS ) MONSANTO CO.
XX
PI  Barry GF;
XX
DR  WPI; 2000-387806/33.
DR  P-PSDB; AAY71251.
XX
PT  Enhancing phosphonate herbicide tolerance in corn, tobacco, wheat,
PT  cotton, canola and rice plants involves transforming plants with •
PT  phosphonate metabolizing genes encoding acyltransferase enzyme.
XX
PS  Disclosure; Page 173-175; 179pp; English.
XX
CC  The patent disclosees a method for selectively enhancing the phosphonate
CC  herbicide tolerance in recombinant corn, tobacco, wheat, cotton, canola
CC  and rice plants, by transforming the plants with an expression cassette.
CC  It comprises of a structural DNA sequence, that encodes an aminomethyl
CC  phosphonic acid (AMPA) acyltransferase or transacylase (AAT), capable of
CC  N-acylation of AMPA. This sequence has an amino terminal chloroplast
CC  transit peptide (CTP), that targets AAT to the chloroplast. Co-expression
CC  of glyphosate oxidase (GOX) gene, encoding glyphosate oxidoreductase,
CC  along with AAT provides the transformed plants with higher resistance to
CC  phosphonate herbicides. This method is useful for enhancing phosphonate
CC  herbicides such as glyphosate and AMPA tolerance, in recombinant plants
CC  and to prevent self-fertilisation and enhance hetero-fertilisation. The
CC  present DNA sequence is the expression cassette-5, comprising a plant
CC  operable promoter and 5' sequences like intron, linked to modified E.
CC  coli phnO coding region, encoding P2A AMPA acyltransferase (AAT) enzyme
CC  and plant operable termination sequences
XX
SQ  Sequence 2436 BP; 634 A; 565 C; 567 G; 670 T; 0 U; 0 Other;

Query Match             75.3%;  Score 554;  DB 3;  Length 2436;
Best Local Similarity   94.5%;  Pred. No. 6.4e-172;
Matches  586;  Conservative   0;  Mismatches  30;  Indels    4;  Gaps    1;

Qy     116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCCGGGAAACCTCCTCCGGATTCCATTGCC 175
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      28 TCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGGAAACCTCCTCCGGATTCCATTGCC 87

```
Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAGGTTGCCACCTACAAATGCC 235
         ||||||||||||||  |||||| ||||||||||||||||||| |   || ||||||
Db    88 CAGCTATCTGTCACTTTATTGTCGAAGATAGTGGAAAAAGGAGGTGGGCTCCTACAAATGCC 147

Qy   236 ATCATTGCGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGTGCCCAAAG 295
         ||||||||||||||||||||||  ||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGAGTTGAGAGTGCCTCTGCCGACAGTGTGCCCAAAG 207

Qy   296 ATGGACCCCACCCACGAGGAGCATCGTGGAAAAAGAGAAGCGTTCCAACCACGTCTTCAA 355
         |||||||  ||| ||||||||||||||||||||||||||||| ||||||| ||||||
Db   208 ATGGACCCCACCCACCACGAGGAGCATCGTGGAAAAAAAGAGAACGACGTTCCAACCACGTCTTCAA 267

Qy   356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
         ||||||||||||||||||||     ||||||||||||||| || ||||||||||||||||
Db   268 AGCAAGTGGATTGATGTGAGGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy   412 AACCTCCTGGATTCCATTGCCCAGCTATCGTCGTCACTTCATCAAAAGGACAGTAGAAAAG 471
         ||||||||||||||||||| ||||||||||||||  ||| |||  ||||||||
Db   328 AACCTCCTGGATTCCATTGCCCAGCTATCGTCACTTATTGTGAAGATAGTGGAAAAG 387

Qy   472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTCAAGATGCC 531
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 GAAGGTGGCTCCTACAAATGCCATCATTGCCGATAAAGGAAAGGCCATCGTTGAAGATGCC 447

Qy   532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
         |||||||||||||||  ||||||||||||||||||||||||||| ||||||||||||||
Db   448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 507

Qy   592 GAGGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATTGAGTGATATCTGACGTAAGG 651
         |||||| ||||||||||||||||  ||||||| ||||| ||||||||||||||||||
Db   508 GAGGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATTGAGTGATATCTGACGTAAGG 567

Qy   652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAATAAGGAAGTTCATTT 711
         |||||||||||||||||||||||||||||||||||  ||| ||| ||||||||||||||
Db   568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATAATAAGGAAGTTCATTT 627

Qy   712 CATTTGGAGGAGGACACGCTG 731
         |||||||||||||||||||||
Db   628 CATTTGGAGGAGGACACGCTG 647
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RESULT 8
```
AEF22504
ID   AEF22504 standard; DNA; 2767 BP.
XX
AC   AEF22504;
XX
DT   23-MAR-2006   (first entry)
XX
DE   RNAi transcription unit with polyadenylation site vector 1A.
XX
KW   ds; gene; Hsp70; heat shock protein 70; luciferase; nopaline synthase;
KW   transgenic plant; RNA interference; gene silencing; pathogen resistance;
KW   plant pest; plant growth regulant; insect resistance; crop improvement.
XX
OS   Cauliflower mosaic virus.
OS   Zea mays.
OS   Agrobacterium tumefaciens.
OS   Chimeric.
XX
FH   Key            Location/Qualifiers
FH
FT   promoter       1..614
FT                  /*tag= a
FT                  /label= CaMV_35S
FT   enhancer       645..1448
FT                  /*tag= b
FT                  /label= zea_mays_Pe35S-Hsp_intron
FT   repeat_region  1025..2502
FT                  /*tag= d
FT                  /rpt_type= INVERTED
FT   CDS            complement(1025..1455)
FT                  /*tag= c
```

```
FT   CDS            /product= "firefly luciferase (LUC)"
FT                  /note= "No start or stop codons shown"
FT                  /partial
FT                  2082..2502
FT                  /*tag= e
FT                  /product= "firefly luciferase (LUC)"
FT                  /note= "No start or stop codons shown"
FT                  /partial
FT                  2515..2767
FT                  /*tag= f
FT   3'UTR          /note= "From Agrobacterium tumefaciens nopaline synthase
FT                  gene"
XX
PN   US2006026711-A1.
XX
PD   02-FEB-2006.
XX
PF   20-JUL-2005; 2005US-00186196.
XX
PR   21-JUL-2004; 2004US-0589643P.
XX
PA   (HUAN/) HUANG S.
PA   (GILB/) GILBERTSON L A.
XX
PI   Huang S, Gilbertson LA;
XX
DR   WPI; 2006-124885/13.
XX
PT   Non-systemic gene suppression comprises transcribing in a transgenic
PT   plant a recombinant DNA construct comprising a promoter operably linked
PT   to a gene suppression element.
XX
PS   Example 1; SEQ ID NO 1; 12pp; English.
XX
CC   The present sequence is that of a synthetic vector produced in the
CC   current invention of a novel method for the non-systemic suppression of a
CC   target gene, comprising transcribing in a transgenic plant a recombinant
CC   DNA construct consisting of a promoter operably linked to a gene
CC   suppression element, producing RNA that non-systemically suppresses a
CC   target gene and is retained in the nucleus, therefore suppressing the
CC   target gene relative to expression in the absence of the transcription.
CC   The RNAi transcriptional unit of vector 1A included (a) a chimeric
CC   promoter including an enhanced CaMV35S promoter linked to an enhancer
CC   element (the maize Pe35S-Hsp intron), (b) an inverted repeat of DNA
CC   coding for firefly luciferase with anti-sense oriented DNA followed by a
CC   sense oriented DNA and (c) a 3'UTR DNA from Agrobacterium tumefaciens
CC   nopaline synthases gene which provides a polyadenylation site. Vector 1A
CC   was electroporated together with reporter vectors for firefly luciferase
CC   and Renilla luciferase into three separate volumes of maize protoplasts.
CC   Suppression experiments were performed to confirm the enhanced ability
CC   for gene suppression exhibited by constructs without a functional
CC   polyadenylation site relative to those with. A target gene is a gene
CC   native to the transgenic plant, a transgene in the transgenic plant. A
CC   gene native to a pest or pathogen of the transgenic plant, or a microRNA
CC   precursor DNA sequence. The promoter is a seed-specific promoter and the
CC   non-systemic suppression is seed-specific suppression of a target gene.
CC   The invention is useful for crop resistance to a pest or pathogen where
CC   the pest is an insect, e.g. a coleopteran, or a nematode, where the
CC   nematode is a root nematode and the tissue-specific promoter is a root-
CC   specific promoter.
XX
SQ   Sequence 2767 BP; 774 A; 569 C; 580 G; 844 T; 0 U; 0 Other;
```

```
Query Match             75.3%;  Score 554;  DB 15;  Length 2767;
Best Local Similarity   94.5%;  Pred. No. 6.8e-172;
Matches  586;  Conservative   0; Mismatches  30; Indels   4;  Gaps   1;

Qy   116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCCATTGCC 175
         ||| ||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db     3 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCCATTGCC 62

Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC 235
         ||||||| ||||  || |||||| ||| ||||||||||||  ||||||||||||
```

```
Db    63 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAAATGCC 122
Qy
Db   236 ATCATTGCGATAAAAGAAAAGGCTATCCTTCAAGATGCCTCTTGCCGACAGTGGTCCCAAG 295
Qy
Db   123 ATCATTGCGATAAAAGAAAAGGCCATCCTTGAAGATGCCTCTTGCCGACAGTGGTCCCAAG 182
Qy
Db   296 ATGGACCCCAGGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCACCACGTCTTCAA 355
Qy
Db   183 ATGGACCCCAGGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCACCACGTCTTCAA 242
Qy
Db   356 AGGCAAGTGGATTGATTCATCGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA 411
Qy
Db   243 AGCAACTGGATTGATTGATTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 302
Qy
Db   412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGGTAATATCCGGA 471
Qy
Db   303 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 362
Qy
Db   472 GAAGGTGGCGACCTACAAAATGCCATCATTGCGATAAAAGGCTATCCTTCAAGATGCC 531
Qy
Db   363 GAAGGTGGCGTCCTACAAAATGCCATCATTGCGATAAAAGAAAAGGCCATCGTTGAAGATGCC 422
Qy
Db   532 TCTCGCGACAGTGGTCCCAAAGATGGACCCCACCCCAGGAGGAGCATCGTGGAAAAAGA 591
Qy
Db   423 TCTCGCGACAGTGGTCCCAAAGATGGACCCCACCCCAGGAGGAGCATCGTGGAAAAAGA 482
Qy
Db   592 GAGGTTCAACACAGTGTTCAAACAGCAGTGGTTGAATTGATGTGATTAATCTCACGGTAAGG 651
Qy
Db   483 GAGGTTCAACACAGTGTTCAAACAGCAGTGGTTGAATTGATGTGATTAATCTCCACTGCAGGTAAGG 542
Qy
Db   652 GATGACGGCACAATCCCAACTACCTTCCTCCTCTATATAAGGAGTTCATTT 711
Qy
Db   543 GATGACGGCACAATCCCAACTACCTTCCTCCGACAAGACCCTTCCTCTCTATATAAGGAGTTCATTT 602
Qy
Qy   712 CAATTGGAGAGGACAGCGCTG 731
Db   603 CAATTGGAGAGGACACGCGCTG 622
```

```
RESULT 9
AA251646
ID    AA251646 standard; DNA; 3469 BP.
XX
AC    AA251646;
XX
DT    15-SEP-2003  (revised)
DT    21-JUN-2000  (first entry)
XX
DE    Bacillus thuringiensis Cry3Bb variant 11231mv2 expression cassette-2.
XX
KW    delta-endotoxin; Cry3B; Bt toxin; crystal protein; insect pest;
KW    insecticide; Coleopteran; expression cassette; transgenic plant;
KW    Cry3BB variant 11231mv2; de.
XX
OS    Bacillus thuringiensis
OS    Cauliflower mosaic virus.
OS    Triticum aestivum.
OS    Oryza sativa.
OS    Chimeric.
XX
FH    Key              Location/Qualifiers
FH
FT    promoter         25..640
FT                     /tag= a
FT                     /label= P-CaMV.35S
FT    5'UTR            664..734
FT                     /tag= b
FT                     /label= L-Ta.hcbi
FT                     /note= "Wheat chlorophyll A/B binding protein
FT                     untranslated leader sequence"
FT    intron           748..1238
FT                     /tag= c
FT                     /label= I-Os.Act1
FT                     /note= "Rice actin intron sequence"
```

```
FT    CDS              1241..3202
FT                     /tag= d
FT                     /product= "Cry3Bb variant 11231mv2"
FT    terminator       3317..3450
FT                     /tag= e
FT                     /label= T-Ta.hsp17
FT                     /note= "Wheat heat shock Hsp17 transcription termination
FT                     and polyadenylation sequence"
```

```
PN    WO20011185-A2.
XX
PD    02-MAR-2000.
XX
PF    19-AUG-1999;  99WO-US018883.
XX
PR    19-AUG-1998;  98US-0097150P.
XX
PA    (MONS ) MONSANTO CO.
XX
PI    Romano CP;
XX
DR    WPI; 2000-246568/21.
DR    P-PSDB; AAY70446.
XX
PS    Claim 16; Page 149-152; 171pp; English.
```

```
CC    The present sequence is an expression cassette from a Cry3Bb plant
CC    expression vector pMON33748. It comprises an enhanced Cauliflower mosaic
CC    virus (CaMV) 35S promoter sequence, a wheat chlorophyll A/B binding
CC    protein untranslated leader sequence, a rice actin intron sequence, a
CC    Bacillus thuringiensis delta-endotoxin Cry3Bb variant 11231mv2 coding
CC    sequence and a wheat heat shock Hsp17 transcription termination and
CC    polyadenylation sequence. This expression cassette is used to improve
CC    expression of Cry3B variant protein in transgenic plants e.g. maize, to
CC    increase insecticidal activity against Coleopteran pests. (Updated on 15-
CC    SEP-2003 to standardise OS field)
XX
SQ    Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;
```

```
Query Match             75.3%;  Score 554;  DB 3;  Length 3469;
Best Local Similarity   94.5%;  Pred. No. 7.6e-172;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;
```

```
Qy   116 TCTCGAGTGCAGACTTTTCAACAAAAGGTAATATCGGAAAACCTCCTCGGATTCCATTGCC 175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28 TCCGAGTGAGACTTTTCAACAAAGGGTAATATCCGGAAAACCTCCTCGGATTCCATTGCC 87
Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGTAAAAGAGAAGGTGGCCACCTACAAAATGCC 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAAATGCC 147
Qy   236 ATCATTGCGATAAAAGAAAAGGCTATCCTTCAAGATGCCTCTTGCCGACAGTGGTCCCAAG 295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAAGAAAAGGCCATCCTTGAAGATGCCTCTTGCCGACAGTGGTCCCAAG 207
Qy   296 ATGGACCCCACCCCAGGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCACCACGTCTTCAA 355
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 ATGGACCCCACCCCAGGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCACCACGTCTTCAA 267
Qy   356 AGCAACTGGATTGATTGATTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA 411
         |||||||||||||||||||||    ||||||||||||||||||||||||||||||||||||
Db   268 AGCAACTGGATTGATTGATTGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGGTAATATCGGAAAG 471
         ||||||||||||||||||||||||||||||||||||||  |||||          ||
Db   328 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
Qy   472 GAAGGTGGCGACCTACAAAATGCCATCATTGCGATAAAAGGCTATCCTTCAAGATGCC 531
         |||||||||||  ||||||||||||||||||||||||  |||||          |||
Db   328 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387
```

```
PT   New transgenic plant resistant to Coleopteran pests, comprises Bacillus
PT   thuringiensis Cry3-delta-endotoxin gene.
XX
PS   Claim 16; Page 77-80; 0pp; English.
XX
CC   The invention relates to novel transgenic plants comprising Bacillus
CC   thuringiensis Cry3-delta-endotoxin gene or its variants having
CC   coleopteran inhibitory activity. The invention is useful for controlling
CC   coleopteran insect infestation in a field of crop plants. The present
CC   sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
CC   vector DNA.
XX
SQ   Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;

Query Match        75.3%;   Score 554;  DB 10;   Length 3469;
Best Local Similarity  94.5%;   Pred. No. 7.6e-172;
Matches  586;  Conservative   0;  Mismatches  30;  Indels   4;  Gaps   1;

Qy    116  TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC  175
           ||||||||||||||||||||| ||||||||||||||||||||| ||||||||||||||||
Db     28  TCCGATGTGAGACTCTTCAACAAAGGGTAATATCCCGGAAACCTCCTCGGATTCCATTGCC   87

Qy    176  CAGCTATCTGTCACTTCATCAAAGGACAGTAGAAAAGGAAGGTGGCACCTACACAAATGCC  235
           |||||||||||| | ||| |||||||||| |||||||||||||||||||||||||||||||
Db     88  CAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAGGAAGGTGGCTCCTACACAAATGCC  147

Qy    236  ATCATTGCGATAAAGGAAAAGGCCATCGTTCAAGATGCCTCTGCCGACAGTGTCCCAAAG  295
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148  ATCATTGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGTCCCAAAG  207

Qy    296  ATGGACCCCACCCAGGAGCATCGTGGAAAAGAAGACGTTCCAACCACGTCTTCAA  355
           ||||||||||||||||||||||||||||||           |||||||||||||||||||
Db    208  ATGGACCCCACCCAGGAGCATCGTGGAAAAGAAGAGCAGACGTTCCAACCACGTCTTCAA  267

Qy    356  AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTCACTCACTCATCAAAAGGTAATATCGGGA  411
           ||||||||||||||||| |||    |||||||||||||||| |||| |||||||||||||||
Db    268  AGCAAGTGGATTGATGTGATGTCCGATGTGAGACTTTCAACAAAGGGTAATATCCCGGA  327

Qy    412  AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTCATCAAAAGGACAGTAGAAAAG  471
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    328  AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGAAAAG  387

Qy    472  GAAGGTGGCACCTACAAAATGCCATCATTGCGATAAAGGAAGGCTAAGTGTTCAAGATGCC  531
           |||||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Db    388  GAAGGTGGCTCCTACACAAATGCCATCATTGCGATAAAGGAAGGCCATCGTTGAAGATGCC  447

Qy    532  TCTGCCGACAGTGTCCCAAAGATGGACCCCACCCAGCCGGAGCATCGTGGAAAAAGAA  591
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    448  TCTGCCGACAGTGTCCCAAAGATGGACCCCACCCAGCCGGAGCATCGTGGAAAAAGAA  507

Qy    592  GACGTTCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG  651
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG  567

Qy    652  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT  711
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT  627

Qy    712  CATTTGGAGAGGACACGCTG  731
           ||||||||||||||||||||
Db    628  CATTTGGAGAGGACACGCTG  647
```

```
RESULT 11
ABX95190
ID   ABX95190 standard; DNA; 3469 BP.
XX
AC   ABX95190;
XX
DT   12-JUN-2003  (first entry)
XX
DE   B. thuringiensis delta endotoxin Cry3Bb1 11231mv2 expression cassette #2.
XX
```

```
Db     388  GAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGATGACCCCACCCAGCCGGAGCATCGTTGAAGATGCC  447
            ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Qy     532  GACGTTCCAACCACCTCTTCAAAGCAAGCAAGTGATTGATGTGATATCTCCACTGACGTAAGG  651
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     448  GACGTTCCAACCACGTCTTCAAAGCAAGCAAGTGATTGATGTGATATCTCCACTGACGTAAGG  567

Qy     652  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT  711
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT  627

Qy     712  CATTTGGAGAGGACACGCTG  731
            ||||||||||||||||||||
Db     628  CATTTGGAGAGGACACGCTG  647
```

```
RESULT 10
AAD61794
ID   AAD61794 standard; DNA; 3469 BP.
XX
AC   AAD61794;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Bt.cry3Bb.11231mv2 expression vector DNA, pMON33748.
XX
KW   Transgenic plant; Cry3Bb-delta-endotoxin; Coleopteran pest resistance;
KW   insecticide; variant; cyclic; circular; chimeric; rice; wheat; gene; ds.
XX
OS   Chimeric - Cauliflower mosaic virus.
OS   Chimeric - Oryza sativa.
OS   Chimeric - Bacillus thuringiensis.
OS   Chimeric - Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   promoter        25..640
FT                   /tag= a
FT                   /note="Cauliflower mosaic virus 35S promoter (P-
FT                   CaMV.35S)"
FT   misc_feature    664..734
FT                   /tag= b
FT                   /note="Wheat chlorophyll A/B binding protein
FT                   untranslated leader sequence (L-Ta.hcb1)"
FT   intron          748..1238
FT                   /tag= c
FT                   /note="Rice actin intron (I-Os.Act1)"
FT   CDS             1241..3202
FT                   /tag= d
FT                   /product= "Bt.cry3Bb.11231mv2 protein"
FT   misc_feature    3217..3420
FT                   /tag= e
FT                   /note= "Wheat heat shock Hsp117 transcription termination
FT                   and polyadenylation sequence (T-Ta.Hsp117)"
XX
PN   US2003115630-A1.
XX
PD   19-JUN-2003.
XX
PF   29-AUG-2002;  2002US-00232665.
XX
PR   19-AUG-1999;  99US-00377466.
XX
PA   (ROMA/) ROMANO C P.
XX
PI   Romano CP;
XX
DR   WPI; 2003-810928/76.
DR   P-PSDB; ABW01055.
XX
```

KW   Cry3Bb1 11z1mv2; gene; delta-endotoxin; plant; transgenic; insecticide;
KW   crystal 3; Cry3; Coleopteran insect infestation; increased toxicity; da;
KW   season long protection; beetle; maize; rice; expression cassette.
XX
OS   Bacillus thuringiensis.
OS   Zea mays.
OS   Oryza sativa.
OS   Cauliflower mosaic virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FH
FT   promoter        25..640
FT                   /*tag= a
FT                   /note= "Enhanced CMV35S promoter"
FT   5'-UTR          664..734
FT                   /tag= b
FT                   /notes "Wheat chlorophyll A/B binding protein
FT                   untranslated leader sequence"
FT   Intron          748..1238
FT                   /*tag= c
FT                   /numbers 1
FT                   /cons_splice (5'site:NO,3'site:NO)
FT                   /note= "Rice actin intron"
FT   CDS             1241..3202
FT                   /*tag= d
FT                   /product= "Cry3Bb1 11z1mv2"
FT   misc_signal     3217..3450
FT                   /*tag= e
FT                   /note= "Wheat heat shock HSP17 transcription terminator
FT                   and polyadenylation sequence"
XX
CC   pathogens is achieved using the modified polynucleotide. The modified
CC   polynucleotide reduces the number of transgenic events that have to be
CC   screened in order to identify one which contains beneficial levels of one
CC   or more insect controlling compositions. The present sequence represents
CC   Bacillus thuringiensis delta endotoxin Cry3Bb1 11z1mv2 expression
CC   cassette #2 DNA
XX
SQ   Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;

Query Match  75.3%;  Score 554;  DB 10;  Length 3469;
Best Local Similarity  94.5%;  Pred. No. 7.6e-172;
Matches 586;  Conservative  0;  Mismatches 30;  Indels  4;  Gaps  1;

Qy  116 TCTGCAGTGAGGACTTTTCAACAAAAGGTAATAATGGGGAAACCTTCTCGGAATTCCATTGCC 175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 TCCGAGTGAGGACTTTTCAACAAAAGGTAATAATGGGGAAACCTTCTCGGAATTCCATTGCC  87

Qy  176 CAGCTACTGTCACTTCATCAAAACGACGACAGTAGAAAAAGAGAAGCGGACCACTTACAAATGCC 235
Db   88 CAGCTACTGTCACTTCATTGTGAAGATAGTGAAAAAGAGAAGCGGACCACTTACAAATGCC 147

Qy  236 ATCATTGCCATAAAAGAAAGGCTATCCTTCAAGATGCCTCTGCCCGACGTGGTCCCAAAG 295
Db  148 ATCATTGCCATAAAAGAAAGGCATCCTTGCCCGACGTGGTCCCAAAG 207

Qy  296 ATCGACCCCCACCCACGACGAGGAGCATCGTCGAAAAAGAAGAGGTTCCAACCACGTCTTCAA 355
Db  208 ATCGACCCCCACCCACGGAGCATCGTCGAAAAAGAAGAGGTTCCAACCACGTCTTCAA 267

Qy  356 AGCAAGTGGATTGGATTGTGAT----TGCACGTGAGGACTTTTCACAAAGGGGTAATATCGGGA 411
Db  268 AGGAAGTGGGATTGATTGTGATGTCCGATGTGAGGACTTTTCACAAAGGGGTAATATCCGGA 327

Qy  412 AACCTTCTCGGAATCCATTGCCCAGCTACTGTCACTTCATCAAAACGACGACAGTAGAAAAG 471
Db  328 AACCTTCTCGGAATCCATTGCCCAGCTACTGTCACTTCATCAAAACGACGACAGTAGAAAAG 387

Qy  472 GAAGGTGGCCACTTACAAAATGCCATCATTGCGATAAAGGAAAAGGCTATCCTTCAAGATGCC 531
Db  388 GAAGGTGGCTCCTTACAAAATGCCATCATTGCGATAAAGGAAAAGGCCATCGTTGGTCAAGAGTCC 447

Qy  532 TCTGCCGACAGTGGTCTCCCAAAAGATGAGACCCCCACCCACGGAGCATCGTCGGAAAAAGAA 591
Db  448 TCTGCCGACAGTGGTCTCCCAAAAGATGAGACCCCCACCCACGGAGCATCGTCGGAAAAAGAA 507

Qy  592 GAGGTTCCAACCACGTCTTCAAAACGAAGGTGGATTGATTGTGATATTCCCACTGACGTAAGG 651
Db  508 GAGGTTCCAACCACGTCTTCAAAACGAAGGTGGATTCGATGTGATATTCCCACTGACGTAAGG 567

Qy  652 GATGACGGCACAATCCCACTATCCTTCGGCAAGACCCTTCCTTATAATAAGGAAGAGTTCATTT 711
Db  568 GATGACGGCACAATCCCACTATCCTTCGGCAAGACCCTTCCTTATAATAAGGAAGAGTTCATTT 627

Qy  712 CATTGGAGAGGACACGCTG 731
Db  628 CATTGGAGAGGACACGCTG 647

---

Disclosure; Col 141-148, 107pp; English.

CC   The invention relates to a modified polynucleotide which encodes an
CC   insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such
CC   as Cry3b. The modified polynucleotide is useful for producing a
CC   transformed maize plant cell and regenerating a maize plant
CC   selecting a transformed maize plant cell. A transgenic plant expressing the
CC   modified polynucleotide is useful for producing a transformed maize plant
CC   by introducing the modified polynucleotide into a maize plant cell,
CC   such as a plant cell (preferably a maize cell) or a microbial cell. The
CC   modified polynucleotide is useful for producing a
CC   modified polynucleotide relative to the highest levels of insect controlling
CC   delta-endotoxin provides up to 10 fold higher levels of insect controlling
CC   polynucleotide provides up to 10 fold higher levels of insect controlling
CC   compositions. In particular, transgenic maize expressing higher levels of
CC   the Cry3Bb protein designed to exhibit increased toxicity toward
CC   Coleopteran pests deliver superior levels of insect protection and are
CC   less likely to sponsor development of populations of target insects that
CC   are resistant to the insecticidally active protein. Improved control of
CC   susceptible target insect pests and season long protection from insect

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RESULT 12
AEB665524
ID   AEB665524 standard; DNA, 3469 BP.
XX
AC   AEB665524;
XX
DT   09-FEB-2006 (first entry)
XX
DE   Bt.cry3Bb1.11z1mv2 expression vector DNA, pMON33748.
XX
KW   crop improvement; transgenic plant; insect resistance; gene expression;
KW   Coleopteran inhibitory activity; insecticide; endotoxin; Cry3Bb; gene;
KW   da; circular; vector; gene fusion; promoter; heat shock protein; intron;
KW   chlorophyll A/B binding protein; actin.
XX

DR   US6501009-B1.
DR   WPI; 2003-352192/33.
DR   P-PSDB; AEU09202.

PA   (MONS ) MONSANTO TECHNOLOGY LLC.
PI   Romano CP;

PF   19-AUG-1999;  99US-00377466.
PR   19-AUG-1999;  99US-00377466.

PN   31-DEC-2002.

PT   New modified polynucleotide useful for controlling Coleopteran insect
PT   infestation in a field of crop plants. The modified polynucleotide is
PT   useful for controlling Coleopteran insect
PT   Bacillus thuringiensis delta-endotoxin.

```
Matches 586;  Conservative 0;  Mismatches 30;  Indels 4;  Gaps 1;

Qy  116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGAAACCTTCCTCGGATTCCATTGCC 175
            || ||||||||| ||||||||||||||||||| |||||||||||||||||||||||
Db   28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTTCCTCGGATTCCATTGCC 87

Qy  176 CAGCTATCGTCACTCATCAAAGGACAGTAGAAAAGGAAGGTGGCACTCACAAAATGCC 235
            |||||||||||||        ||  || ||||| ||||||||||||| || ||||||||
Db   88 CAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAATGGAAAAGGAAGGTGGCTCCTACAAAATGCC 147

Qy  236 ATCATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
            ||||||| |||||||||||||| |||||| |||||||||| |||||||||||||||||||
Db  148 ATCATTGGATAAAGGAAAGGCCATCGTTGAAGATGCCTCGGCCGACAGTGGTCCCAAAG 207

Qy  296 ATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGAAGACGTTCAACCACGTCTTCAA 355
            |||||||||||||||||||||||||||||||||||||| |||||||| |||||||||||
Db  208 ATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGAAGAAGACGTTCCAACCACGTCTTCAA 267

Qy  356 AGCAAGTGGATTGATCGTGAT----TGCCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA 411
            ||||||||||||||| |||||    ||| ||| |||| |||||  ||||||||||||||||||
Db  268 AGCAAGTGGATTGATTGCAGATGTCACTTGTCACTTTATTGTGAAGATAGTGGAAAAG 327

Qy  412 AACTTCCTCGGATTCCAGTCACTCGTCACTCATCAAAGACAGTAGAAAG 471
            ||||||||| |||||||| |||||||| ||||||| ||||| |||| |||
Db  328 AACTTCCTCGGATTCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387

Qy  472 GAAGGTGGCACTACAAATGCCATCATTGGGATAAATGCCATCATTGGTCGTTCGTTGAAGATGCC 531
            |||||||||| |||||||||||||||||| |||| ||||||||||  ||||  |||| ||||||||
Db  388 GAAGGTGGCTCCTACAAATGCCATCATTGGGATAAAGGCCATCATTGGTGAAGATGCC 447

Qy  532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGA 591
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCAGGAGGACATCGTGGAAAAAGA 507

Qy  592 GACGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 651
            ||||||||||||||||||||| |||||||||||||||||||| |||||||||||||||||
Db  508 GACGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 567

Qy  652 GATGACGCACAATCCCAGTATCCTTCGGCCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
            ||||||||||||| |||||||||||||||||||||||||||||| |||||||||||||||||
Db  568 GATGACGCACAATCCCAGTATCCTTCGGCCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy  712 CATTTGGAGAGGACACGCGTG 731
            |||||||||||||||||||||
Db  628 CATTTGGAGAGGACACGCGTG 647
```

OS   Cauliflower mosaic virus.
OS   Bacillus thuringiensis.
OS   Triticum aestivum.
OS   Oryza sativa.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   promoter        25..640
FT                   /*tag= a
FT                   /note= "Cauliflower mosaic virus 35S promoter (P-CaMV.35S)"
FT   5'UTR           664..734
FT                   /*tag= b
FT                   /note= "Wheat chlorophyll A/B binding protein untranslated leader sequence (L-Ta.hcb1)"
FT   intron          748..1238
FT                   /*tag= c
FT                   /note= "Rice actin intron sequence (I-Os.Act1)"
FT   CDS             1241..3202
FT                   /*tag= d
FT                   /product= "Bacillus thuringiensis Cry3Bb delta-endotoxin 11231mv2 variant protein"
FT   misc_feature    3217..3450
FT                   /*tag= e
FT                   /note= "Wheat heat shock protein 17 transcription termination and polyadenylation sequence (T-Ta.Hsp17)"
XX
PN   US2005273882-A1.
XX
PD   08-DEC-2005.
XX
PF   29-JUL-2005; 2005US-00192801.
XX
PR   19-AUG-1999; 99US-00377466.
PR   29-AUG-2002; 2002US-00232665.
XX
PA   (ROMA/) ROMANO C P.
XX
PI   Romano CP;
XX
DR   WPI; 2006-028189/03.
DR   P-PSDB; AEE66525.
XX
PT   New expression cassette, useful for expressing in transformed plants variant Cry3 Bacillus thuringiensis delta-endotoxins having significant Coleopteran inhibitory activity.
XX
PS   Disclosure; SEQ ID NO 23; 107pp; English.
XX
CC   The present invention discloses methods and compositions comprising a group of novel expression cassettes which provide significantly improved levels of accumulation of Coleopteran inhibitory Cry3B and Cry3B variant amino acid sequences when these are expressed in plants. In particular, the invention relates to a transgenic maize expressing higher levels of a protein designed to exhibit increased toxicity towards Coleopteran pests deliver superior levels of insect protection and are less likely to sponsor development of populations of target insects that are resistant to the insecticidally active protein. Expression cassettes of the invention are useful for expressing in transformed plants variant Cry3 Bacillus thuringiensis delta-endotoxins having significant Coleopteran inhibitory activity. The present sequence is a B. thuringiensis Cry3Bb-delta-endotoxin variant expression vector DNA. This vector DNA comprises a cauliflower mosaic virus 35S promoter (P-CaMV.35S), wheat chlorophyll A/B binding protein untranslated leader sequence (L-Ta.hcb1), rice actin intron sequence (I-Os.Act1), B. thuringiensis Cry3Bb delta-endotoxin 11231mv2 variant coding sequence and wheat heat shock protein (Hsp) 17 transcription termination and polyadenylation sequence (T-Ta.Hsp17).
XX
SQ   Sequence 3469 BP; 790 A; 1078 C; 845 G; 756 T; 0 U; 0 Other;

Query Match              75.3%;  Score 554;  DB 15;  Length 3469;
Best Local Similarity    94.5%;  Pred. No. 7.6e-172;

RESULT 13
AA251642
ID   AA251642 standard; DNA; 3754 BP.
XX
AC   AA251642;
XX
DT   15-SEP-2003  (revised)
DT   21-JUN-2000  (first entry)
XX
DE   Bacillus thuringiensis Cry3Bb variant v11231 expression cassette-2.
XX
KW   delta-endotoxin; Cry3B; Bt toxin; crystal protein; insect pest;
KW   insecticide; Coleopteran; expression cassette; transgenic plant;
KW   Cry3Bb variant v11231; ds.
XX
OS   Cauliflower mosaic virus.
OS   Zea mays.
OS   Bacillus thuringiensis.
OS   Agrobacterium tumefaciens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   promoter        25..640
FT                   /*tag= a
FT                   /label= CaMV35S_promoter
FT   intron          669..1472

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FT
FT   CDS
FT            /tag= b
FT            /label= I-Zm.Hsp70
FT            /note= "Zea mays Hsp70 intron sequence"
FT            1490. .3451
FT            /tag= c
FT   terminator
FT            /product= "Cry3Bb variant AAV1231"
FT            3475. .3730
FT            /tag= d
FT            /label= T-AGRtu.nos
FT            /note= "Agrobacterium tumefaciens nopaline synthase 3'
FT            transcription termination and polyadenylation sequence"
XX
XX
PN   WO200011185-A2.
XX
PD   02-MAR-2000.
XX
PF   19-AUG-1999;   99WO-US018083.
XX
PR   19-AUG-1998;   98US-0097150P.
XX
PA   (MONS ) MONSANTO CO.
XX
PI   Romano CP;
XX
DR   WPI; 2000-246568/21.
DR   P-PSDB; AAY70444.
XX
PT   Novel expression cassettes which express Bacillus thuringiensis Cry3
PT   delta-endotoxin portion which is toxic to coleopteran insect pests,
PT   useful for producing transgenic plants with improved insecticidal
PT   activity.
XX
PS   Claim 16; Page 125-128; 171pp; English.
XX
CC   The present sequence is an expression cassette from a Cry3Bb plant
CC   expression vector pMON33710. It comprises an enhanced Cauliflower mosaic
CC   virus (CaMV) 35S promoter sequence, a maize Hsp70 intron sequence, a
CC   Bacillus thuringiensis delta-endotoxin Cry3Bb variant AAV1231 coding
CC   sequence and a nopaline synthase transcription termination and
CC   polyadenylation sequence. This expression cassette is used to improve
CC   expression of Cry3B variant protein in transgenic plants e.g. maize, to
CC   increase insecticidal activity against Coleopteran pests. (Updated on 15-
CC   SEP-2003 to standardise OS field)
XX
SQ   Sequence 3754 BP; 1030 A; 889 C; 1035 T; 0 U; 0 Other;

Query Match             75.3%;  Score 554; DB 3;  Length 3754;
Best Local Similarity   94.8%;  Pred. No. 7.9e-172;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy          116 TCTGCAGTTGAGACTTTTCAACAAAGGGTAATTATCCGGACAACCTCGGAATTCCATTGCC 175
                ||  | ||||||||||| |||||||||||| |||||||  ||||||||||||||||||||
Db           28 TCCGAGTGAGACTTTTCAACAAAGGGTAATTATCCGGACAATTCCATTGCC 87

Qy          176 CAGCTATCTTGTCACTTATTGTGTAGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCC 235
                |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db           88 CAGCTATCTTGTCACTTATTGTGTAGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCC 147

Qy          236 ATCATTGCGATAAAGGAAAAGGGCTATCGTTCAAGATGCCTTCTGCCGACAGTGGTCCCAAAG 295
                ||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db          148 ATCATTGCGATAAAGGAAAAGGGCTATCGTTCAAGATGCCTTCTGCCGACAGTGGTCCCAAAG 207

Qy          296 ATGGACCCCCACCACCAGGAGCACGTCGTGAAAAAGAGAGAGGTTCAACCACGTCTTCAA 355
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          208 ATGGACCCCCACCACCAGGAGCACGTCGTGAAAAAGAGAGGTTCAACCACGTCTTCAA 267

Qy          356 AGCAAGTGGATTGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATACCGGA 411
                ||||||||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db          268 AGCAAGTGGATTGATTGATGTGATGTCGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy          412 AACCTCCTCGGAATTCCATTGCCCAGCTATCTGTCACTTATTGTGTAGAAGATAGTGAAAAG 471
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          328 AACCTCCTCGGAATTCCATTGCCCAGCTATCTGTCATCAAAAGCAGACAGTGAGAAAAG 387
```

RESULT 14
```
ID   AAD61790 standard; DNA; 3754 BP.
XX
AC   AAD61790;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Bt.cry3Bb.v11231 expression vector DNA, pMON33710.
XX
KW   Transgenic plant; Cry3Bb-delta-endotoxin; Coleopteran pest resistance;
KW   insecticide; variant; cyclic; circular; chimeric; maize; gene; ds.
XX
OS   Chimeric  -  Cauliflower mosaic virus.
OS   Chimeric  -  Zea mays.
OS   Chimeric  -  Bacillus thuringiensis.
OS   Chimeric  -  Agrobacterium tumefaciens.
XX
FH   Key            Location/Qualifiers
FH
FT   promoter       25. .640
FT                  /tag= a
FT                  /note= "Cauliflower mosaic virus 35S promoter (P-
FT                  CaMV.35s)"
FT   intron         669. .1472
FT                  /tag= b
FT                  /note= "Zea mays Hsp70 intron (I-Zm.Hsp70)"
FT                  1490. .3451
FT                  /tag= c
FT   CDS            /product= "Bt.cry3Bb.v11231 protein"
FT                  3475. .3730
FT                  /tag= c
FT   misc_feature   /note= "Agrobacterium tumefaciens nopaline synthase
FT                  transcription termination and polyadenylation sequence (T
FT                  -AGRtu.nos)"
XX
XX
PN   US2003115630-A1.
XX
PD   19-JUN-2003.
XX
PF   29-AUG-2002;  2002US-00232665.
XX
PR   19-AUG-1999;  99US-00377466.
XX
PA   (ROMA/ ) ROMANO C P.
XX
PI   Romano CP;
XX
DR   WPI; 2003-810928/76.
DR   P-PSDB; ABW01053.
XX
PT   New transgenic plant resistant to coleopteran pests, comprises Bacillus
```

Db          472 GAAGGTGGCACTTACAAATGCCATCATTGCCGATAAAGGAAAAGGCTATCGTTCAAAGATGCC 531
Db          388 GAAGGTGGTCCTTCTACAAATGCCATCATTGCCGATAAAGGAAAAGGCCCATCGTTGAAGATGCC 447
Db          532 TCTGCCCACAGTGAGGTCCCCAAAGATATGACCCCCACCACCAGGAGCACGTGTGAAAAAGAA 591
Db          448 TCTTGCCCACAGTGTGGTCCAAAGATGACCCCCACCACCAGGAGCACGTGTGGAAAAAGAA 507
Db          592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATTGATGATATCTCCACTGACCTAAGG 651
Db          508 GACGTTCCAACCACGTCTTCAAACCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567
Db          652 GATGACGGACCAATCCCACTATCCTTCGGACAAGACCCTTCTCTTATATAAGGAAGTTCATTT 711
Db          568 GATGACGGACCAATCCCACTATCCTTCGGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627
Db          712 CATTTGGAGAGGACAGCGCTG 731
Db          628 CATTTGGAGAGGACAGCGCTG 647

PT   .thuringiensis Cry3-delta-endotoxin gene.
XX
PS   Claim 16; Page 57-60; 0pp; English.
XX
CC   The invention relates to novel transgenic plants comprising Bacillus
CC   thuringiensis Cry3-delta-endotoxin gene or its variants having
CC   Coleopteran inhibitory activity. The invention is useful for controlling
CC   Coleopteran insect infestation in a field of crop plants. The present
CC   sequence is B. thuringiensis Cry3Bb-delta- endotoxin variant expression
CC   vector DNA
XX
SQ   Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;

     Query Match             75.3%;  Score 554;  DB 10;  Length 3754;
     Best Local Similarity   94.5%;  Pred. No. 7.9e-172;
     Matches  586;  Conservative   0;  Mismatches  30;  Indels  4;  Gaps   1;

Qy       116 TCTGCGACTGAGACTTTCAACAAAGGTAATATCGGAAACCTCCTCGGATTCCATTGCC 175
             |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        28 TCCGATGTGAGACTTTTCAACAAAGGTAATATCCGAAACCTCCTCGGATTCCATTGCC 87

Qy       176 CAGCTATCTGTCACTTCATCAAAAGGACAGGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
             |||||||||| ||| ||||||||  | ||||  |||||||||||||||||||||||||||
Db        88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCC 147

Qy       236 ATCATTGCGATAAAGGAAGGCCATCGTTGAAGATGCCCTGCCCACCAGTGGTCCCAAAG 295
             |||||||||||||||||||||||||  ||||  ||||||||||||||||||||||||||
Db       148 ATCATTGCGATAAAGGAAGGCCATCGTTGAAGATGCCCTGCCCGACAGTGGTCCCAAAG 207

Qy       296 ATGGACCCCCACCCAGGAGGACCATCGTTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
             |||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db       208 ATGGACCCCCCACCCAGGAGGACCATCGTTGGGAAAAAGAAGAAGCGTTCCAACCACGTCTTCAA 267

Qy       356 AGCAAGTGGATTGATGTGAT------TGCAGTGAGACTTTTCAACAAAGGTAATATCGGGA 411
             ||||||||||||||||||||       |||||||||||||||||||||||||||||   |
Db       266 AGCAAGTGGATTGATGTGATGTGATGTCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy       412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCCAAACAAAGGACCAGTGAAAAAG 471
             |||||||||||||||||||||||||||||||| ||||| ||  ||  ||||||||||||||
Db       328 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTGTCACTTTATTGTGAAGATAGTAGTGGAAAAG 387

Qy       472 GAAGGTGGCACCTACAAATGCCATCATTGCCGATAAAGGAAGGCTATCGTTCGTTCCAAGCATGCC 531
             ||||||||||||||| ||| |||||||||||||||||||||||||||||||||||||||||||||
Db       388 GAAGGTGGCTCCTACAAATGCCATCATTGCCGATAAAGGAAGGCCATCGTTGAAGATGCC 447

Qy       532 TCTGCCGACAGTGGTCCCAAAGATGACCCCCACCCACCAGGAGGAGCATCGTGGAAAAAGAA 591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       448 TCTGCCGACAGTGGTCCCAAAGATGACCCCCACCCACCAGGAGGAGCATCGTGGAAAAAGAA 507

Qy       592 GACGTTCCAACCACGTCTTCAAAAGCAAGTGATTGATGATGAAGCAAGTGATGTGAATCCACGACCTAAGG 651
             ||||||||||||||||||||||  ||||| ||||||  | ||||| ||||||||||||||
Db       508 GACGTTCCAACCACGTCTTCAAAGCAAGTGATTGATGATGAATATTCCACGACCTAAGG 567

Qy       652 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCTCTATATAAGGAAGTTCATTT 711
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       568 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy       712 CATTTGGAGGAGGACACGCTG 731
             |||||||||||||||||||||
Db       628 CATTTGGAGGAGGACACGCTG 647

RESULT 15
ABX95186
ID   ABX95186 standard; DNA; 3754 BP.
XX
AC   ABX95186;
XX
DT   12-JUN-2003  (first entry)
XX
DE   B. thuringiensis delta endotoxin Cry3Bbvil1231 expression cassette #2.
XX
KW   Cry3Bbvil1231; ds; gene; delta-endotoxin; plant; transgenic; insecticide;

KW   crystal 3; Cry3; Coleopteran insect infestation; increased toxicity;
KW   season long protection; beetle; maize; expression cassette.
XX
OS   Bacillus thuringiensis.
OS   Zea mays.
OS   Agrobacterium tumefaciens.
OS   Cauliflower mosaic virus.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT
FT   promoter        25..640
FT                   /*tag= a
FT                   /note= "Enhanced CaMV35S promoter"
FT   intron          669..1472
FT                   /*tag= b
FT                   /number= 1
FT                   /cons_splice (5'site:NO,3'site:NO)
FT                   /note= "Zea mays HSP70 intron"
FT   CDS             1490..3451
FT                   /*tag= c
FT                   /product= "Cry3Bbvil1231"
FT   misc_signal     3475..3730
FT                   /*tag= d
FT                   /note= "Agrobacterium tumefaciens nopaline synthase
FT                   transcription terminator and polyadenylation sequence"
XX
RN   US6501009-B1.
PN
XX
PD   31-DEC-2002.
XX
PP   19-AUG-1999;    99US-00377466.
XX
PR   19-AUG-1999;    99US-00377466.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Romano CP;
XX
DR   WPI; 2003-352192/33.
DR   P-PSDB; ABU09198.
XX
PT   New modified polynucleotide useful for controlling Coleopteran insect
PT   infestation in a field of crop plants encodes insecticidal crystal 3
PT   Bacillus thuringiensis delta-endotoxin.
XX
PS   Disclosure; Col 105-110; 107pp; English.
XX
CC   The invention relates to a modified polynucleotide which encodes an
CC   insecticidal crystal 3 (Cry3) Bacillus thuringiensis delta-endotoxin such
CC   as Cry3Bb. The modified polynucleotide is useful for producing a
CC   transformed cell, by introducing the modified polynucleotide into a cell
CC   such as a plant cell (preferably a maize cell) or a microbial cell. The
CC   modified polynucleotide is useful for producing a transformed maize plant
CC   by introducing the modified polynucleotide into a maize plant cell,
CC   selecting a transformed maize plant cell and regenerating a maize plant
CC   from the transformed maize plant cell. A transgenic plant expressing the
CC   modified polynucleotide is useful for controlling Coleopteran insect
CC   infestation in a field of crop plants. The modified polynucleotide is
CC   useful for producing transgenic plants expressing higher levels of the
CC   insect controlling B. thuringiensis delta-endotoxin. The modified
CC   polynucleotide provides up to 10 fold higher levels of insect controlling
CC   delta-endotoxin relative to the highest levels obtained using prior
CC   compositions. In particular, transgenic maize expressing higher levels of
CC   the Cry3Bb protein designed to exhibit increased toxicity toward
CC   Coleopteran pests deliver superior levels of insect protection and are
CC   less likely to sponsor development of populations of target insects that
CC   are resistant to the insecticidally active protein. Improved control of
CC   susceptible target insect pests and season long protection from insect
CC   pathogens is achieved using the modified polynucleotide. The modified
CC   polynucleotide reduces the number of transgenic events that have to be
CC   screened in order to identify one which contains beneficial levels of one
CC   or more insect controlling compositions. The present sequence represents
CC   Bacillus thuringiensis delta endotoxin Cry3Bbvil1231 expression cassette

```
CC   #2 DNA
XX
SQ   Sequence 3754 BP; 1030 A; 889 C; 800 G; 1035 T; 0 U; 0 Other;

Query Match            75.3%;  Score 554; DB 10;  Length 3754;
Best Local Similarity  94.5%;  Pred. No. 7.9e-172;
Matches  586;  Conservative   0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy    116 TCTGCAGTGAGGACTTTCAACAAAGAGGGTAATATCGGGGAACCTCCTCCGGATTCCATTGCC 175
          ||  ||||||||| ||||||||||||||||||||||||   |||||||||||||||||||||
Db     28 TCCGAGTGAGGACTTTTCAACAAAGAGGGTAATATCCCGGAACCTCCTCCGGATTCCATTGCC 87

Qy    176 CAGCTATCTGTCACTTCATCCAAAAGGACGAGCTAGAAAAAGGACGGAAAAGGATTGGCCACCTACAAAATGCC 235
          ||||||||||||||||  || ||||| ||| ||||| |||||||| |||||| |||  |||||||||||||||
Db     88 CAGCTATCTGTCACTTTATTGTCGAGATAGTGGAAAAGGAGGTGGCCTCCTACAAAATGCC 147

Qy    236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTCCGGCGACAGTGGTCCCAAAG 295
          |||||| ||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db    148 ATCATTGCGATAAAGGAAAGGCCCATCGTTGAAGATGCCTCGGCGGACAGTGGTCCCAAAG 207

Qy    296 ATGGACCCCCACCCACGAGGAGCACCTGTGGAAAAAAGAGAGGTTCACCACGGTCTTCAA 355
          ||||||||||||||||||||||||||  ||||| |||||||||||||||||||||||||||
Db    208 ATGGACCCCCACCCACGAGGAGCACGTCGTTGAAAAAGAGAGGTTCACCACGGTCTTCAA 267

Qy    356 AGCAAGTGATTGATTGATTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
          |||||||||||||||||||||     | ||||||||||||||||||||||||||||||||| ||
Db    268 AGCAAGTGATTGATTGATTGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy    412 AACCTCCTCGGATTCCATTGCCCCAGCTATTCTGTCACTCAATCAAAAGGACAGTAGAAAAG 471
          ||||||||||||| ||||||||||||||| |||||||| ||||| ||||| |||||  ||||
Db    328 AACCTCCTCGGATTCCATTGCCCCAGCTATTCTGTCACTTATTGTCGAAGATAGTGGAAAAG 387

Qy    472 GAAGGTGGCCACCTACAAAATGCCATCATTGCGGATAAAAGGGCTATCGTTCAAGATGCC 531
          |||||||||||||||||||||||||||||||| ||||||  ||||||||||||||||||||
Db    388 GAAGGTGGCTCCTACAAAATGCCATCATTGCGATAAAAGGGCCATCGTTGAAGATGCC 447

Qy    532 TCTGCCGACGTGGTCCCAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
          |||| |||||||||||||| |||||||||||||||||||||||||| ||||||||||||
Db    448 TCTGCCGACGTGGTCCCAAAGATGGACCACCCACCACGAGGAGCATCGTGGAAAAAGAA 507

Qy    592 GACGTTCCAACCACGTCTTCAAAGCAAGTGATTGAATGTGATTATCTCCACTGACGTAAGG 651
          |||||||||||||||||||||||||||||||| |||||||| | ||||||||||||||||||
Db    508 GACGTTCCAACCACGTCTTCAAAGCAAGTGATTGAATGTGATTATCTCCACTGACGTAAGG 567

Qy    652 GATGACCCACAATCCCACTATCCTTCGCAGACCCTTCCTCTCTAATATAAGGAAGTTCATTT 711
          |||||||| |||||||||||||||||| ||||| |||||||||||||||||||||||||||||
Db    568 GATGACGCAGATCCCACTATCCTTCGCAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy    712 CATTTGGAGAGGACACGCTG 731
          |||||||||||||||||||
Db    628 CATTTGGAGAGGACACGCTG 647

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OM nucleic - nucleic search, using sw model

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            4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
            5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
            6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
            7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
            8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
            9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
           10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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## SUMMARIES

| Result No. | Score | %Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 554 | 75.3 | 661 | 3 | US-09-027-998A-33 | Sequence 33, Appl |
| 2 | 554 | 75.3 | 661 | 3 | US-09-943-652-33 | Sequence 33, Appl |
| 3 | 554 | 75.3 | 2107 | 3 | US-09-441-340-29 | Sequence 29, Appl |
| 4 | 554 | 75.3 | 2122 | 3 | US-09-441-340-25 | Sequence 25, Appl |
| 5 | 554 | 75.3 | 2436 | 3 | US-09-441-340-31 | Sequence 31, Appl |
| 6 | 554 | 75.3 | 3469 | 3 | US-09-377-466B-23 | Sequence 23, Appl |
| 7 | 554 | 75.3 | 3469 | 3 | US-09-377-466B-15 | Sequence 15, Appl |
| 8 | 554 | 75.3 | 3754 | 3 | US-10-232-665-23 | Sequence 23, Appl |
| 9 | 554 | 75.3 | 3754 | 3 | US-10-232-665-15 | Sequence 15, Appl |
| 10 | 554 | 75.3 | 8012 | 3 | US-09-182-117-1 | Sequence 1, Appl |
| 11 | 554 | 75.3 | 8012 | 3 | US-09-434-039A-1 | Sequence 1, Appl |
| 12 | 554 | 75.3 | 8349 | 3 | US-09-186-002-16 | Sequence 16, Appl |
| 13 | 554 | 75.3 | 8418 | 3 | US-09-182-117-5 | Sequence 5, Appl |
| 14 | 554 | 75.3 | 8418 | 3 | US-09-434-039A-5 | Sequence 5, Appl |
| 15 | 554 | 75.3 | 8798 | 3 | US-09-182-117-4 | Sequence 4, Appl |
| 16 | 554 | 75.3 | 8798 | 2 | US-09-434-039A-4 | Sequence 4, Appl |
| 17 | 551.4 | 74.9 | 1030 | 3 | US-07-936-163-46 | Sequence 46, Appl |
| 18 | 551.4 | 74.9 | 1030 | 3 | US-08-729-601A-43 | Sequence 43, Appl |
| 19 | 551.4 | 74.9 | 1196 | 3 | US-08-729-601A-46 | Sequence 46, Appl |
| 20 | 551.4 | 74.9 | 5897 | 3 | US-09-097-319A-26 | Sequence 26, Appl |
| 21 | 551.4 | 74.9 | 5897 | 3 | US-09-643-971-26 | Sequence 26, Appl |
| 22 | 550.4 | 74.8 | 9335 | 3 | US-09-097-319A-19 | Sequence 19, Appl |
| 23 | 550.4 | 74.8 | 9335 | 3 | US-09-643-971-19 | Sequence 19, Appl |
| 24 | 550 | 74.7 | 10249 | 3 | US-09-186-002-14 | Sequence 14, Appl |
| 25 | 550 | 74.7 | 10339 | 3 | US-09-186-002-13 | Sequence 13, Appl |
| 26 | 548.4 | 74.5 | 10160 | 3 | US-09-097-319A-8 | Sequence 8, Appl |
| 27 | 548.4 | 74.5 | 10160 | 3 | US-09-643-971-8 | Sequence 8, Appl |
| 28 | 548.4 | 74.5 | 11784 | 3 | US-09-097-319A-9 | Sequence 9, Appl |
| 29 | 548.4 | 74.5 | 11784 | 3 | US-09-643-971-9 | Sequence 9, Appl |
| 30 | 548.4 | 74.5 | 11991 | 3 | US-09-097-319A-10 | Sequence 10, Appl |
| 31 | 548.4 | 74.5 | 11991 | 3 | US-09-643-971-10 | Sequence 10, Appl |
| 32 | 543.6 | 73.9 | 4149 | 3 | US-09-377-466B-13 | Sequence 13, Appl |
| 33 | 543.6 | 73.9 | 4149 | 3 | US-10-232-665-13 | Sequence 13, Appl |
| 34 | 534.6 | 72.6 | 5767 | 3 | US-09-810-861B-3 | Sequence 3, Appl |
| 35 | 534.6 | 72.6 | 14446 | 3 | US-09-810-861B-4 | Sequence 4, Appl |
| 36 | 526 | 71.5 | 12614 | 3 | US-09-577-424-1 | Sequence 1, Appl |
| 37 | 514.4 | 69.9 | 10252 | 3 | US-09-186-002-15 | Sequence 15, Appl |
| 38 | 505.6 | 68.7 | 5033 | 2 | US-08-038-768A-1 | Sequence 7, Appl |
| 39 | 476.8 | 64.8 | 2728 | 3 | US-08-836-402B-7 | Sequence 8, Appl |
| 40 | 459.2 | 62.4 | 1138 | 3 | US-09-011-151-8 | Sequence 9, Appl |
| 41 | 459.2 | 62.4 | 1138 | 3 | US-09-011-151-9 | Sequence 9, Appl |
| 42 | 459 | 62.4 | 1742 | 3 | US-09-737-698B-30 | Sequence 30, Appl |
| 43 | 459 | 62.4 | 1742 | 3 | US-09-737-626A-30 | Sequence 30, Appl |
| 44 | 459 | 62.4 | 1742 | 3 | US-10-427-169-30 | Sequence 30, Appl |
| 45 | 459 | 62.4 | 1742 | 3 | US-10-427-180-30 | Sequence 30, Appl |

## ALIGNMENTS

```
RESULT 1
US-09-027-998A-33
; Sequence 33, Application US/09027998A
; Patent No. 6284949
; GENERAL INFORMATION:
;   APPLICANT: Fischhoff, David A
;   APPLICANT: Fuchs, Roy L
;   APPLICANT: Perlak, Frederick J
;   TITLE OF INVENTION: Insect Resistant Plants
;   NUMBER OF SEQUENCES:  54
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Arnold White and Durkee
;     STREET:  PO Box 4433
;     CITY:  Houston
;     STATE:  TX
;     COUNTRY:  USA
;     ZIP:  77210-4433
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/027,998A
;     FILING DATE:  23-FEB-1998
;     CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Patterson, Melinda L
;     REGISTRATION NUMBER:  33,062
;     REFERENCE/DOCKET NUMBER:  MOBT:195
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (713) 787-1400
; INFORMATION FOR SEQ ID NO:  33:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  661 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
US-09-027-998A-33

Query Match             75.3%;  Score 554;  DB 3;  Length 661;
Best Local Similarity   94.5%;  Pred. No. 1.4e-175;
Matches  586;  Conservative   0;  Mismatches  30;  Indels   4;  Gaps   1;

Qy    116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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## Left column

RESULT 2
US-09-943-692-33
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; Sequence 33, Application US/09943692
; Patent No. 6953835
; GENERAL INFORMATION:
; APPLICANT: FISCHHOFF, DAVID A.
; APPLICANT: FUCHS, ROY L.
; APPLICANT: LAVRIK, PAUL B.
; APPLICANT: McPHERSON, SYLVIA A.
; APPLICANT: PERLAK, FREDERICK J.
; TITLE OF INVENTION: COLEOPTERAN TOXIN PROTEINS OF BACILLUS THURINGIENSIS
; FILE REFERENCE: MOBT.195---1
; CURRENT APPLICATION NUMBER: US/09/943,692
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/027,998
; PRIOR FILING DATE: 1998-02-23
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 33
; LENGTH: 661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Cauliflower Mosaic Viral Promoter (CaMV35S)
US-09-943-692-33
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Query Match 75.3%; Score 554; DB 3; Length 661;
Best Local Similarity 94.5%; Pred. No. 1.4e-175;
Matches 586; Conservative 0; Mismatches 30; Indels 4; Gaps 1;

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Qy      20 TCGGATGTCGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 79
Db      20 ...
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(DNA sequence alignment Qy/Db rows, positions 20 through 639)

## Right column

RESULT 3
US-09-441-340-29
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; Sequence 29, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
;
; SEQ ID NO 29
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant operable promoter linked
; OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
; OTHER INFORMATION: acetyltransferase, and termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(590)
; FEATURE:
; NAME/KEY: 5'UTR
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(DNA sequence alignment Qy/Db rows, positions 20 through 639)

; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Descripion of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
US-09-441-340-25

Query Match      75.3%;   Score 554;  DB 3;  Length 2122;
Best Local Similarity  94.5%;   Pred. No. 2.7e-175;
Matches  586;  Conservative   0;  Mismatches   30;  Indels  4;  Gaps  1;

Qy   116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
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Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
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Db    68 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCCTCTACAAATGCC 127

Qy   236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
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Db   128 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG 187

Qy   296 ATGGACCCCACCCACGAGGAGCATCGTCGTGGAAAAAGAAGACGTTCAACCACGTCTTCAA 355
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Db   188 ATGGACCCCACCCACGAGGAGCATCGTCGTGGAAAAAGAAGAAGACGTTCAACCACGTCTTCAA 247

Qy   356 AGCAAGTGGATTGGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
             ||||||||||||||||||||||        ||||||||||||||||||||||||||||||||
Db   248 AGCAAGTGGATTGATGTGATGATGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 307

Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGGACTAGAAAAG 471
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db   308 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAAG 367

Qy   472 GAAGGTGGCACCTACAAATGCCATCATTGCCGATAAAGGCCATCGTTCAAGATGCC 531
             ||||||||||||||||||||||||||||| ||||||||||| ||||||||||||||||||
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Qy   532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCACCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
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Db   488 GACGTTCAACCACGTCTTCAAAAGCAAGTGGATTGATGATATCTCCACTGACGTAAGG 547

RESULT 4
US-09-441-340-25
; Sequence 25, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340

; LOCATION: (615)..(685)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (699)..(1148)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1149)..(1426)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1427)..(1858)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1669)..(2102)
US-09-441-340-29

Query Match      75.3%;   Score 554;  DB 3;  Length 2107;
Best Local Similarity  94.5%;   Pred. No. 2.7e-175;
Matches  586;  Conservative   0;  Mismatches   30;  Indels  4;  Gaps  1;

Qy   116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87

Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
             ||||||||||||| |  |||||||||||||||||||||||||||||||||||||||||||
Db    88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCCTCTACAAATGCC 147

Qy   236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 295
             |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCGCCGACAGTGGTCCCAAAG 207

Qy   296 ATGGACCCCACCCACGAGGAGCATCGTCGTGGAAAAAGAAGACGTTCAACCACGTCTTCAA 355
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 ATGGACCCCACCCACGAGGAGCATCGTCGTGGAAAAAGAAGAAGACGTTCAACCACGTCTTCAA 267

Qy   356 AGCAAGTGGATTGGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
             |||||||||||||||||||||||        ||||||||||||||||||||||||||||||||
Db   269 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCCATCATTGCGATAAAATGCCATCATTGCCGATAAAG 471
             |||||||||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||
Db   328 AACCTCCTCGGATTCCATTGCCCAGCTATCCATCATTGCGATAAAATGCCATCATTGCCGATAAAG 387

Qy   472 GAAGGTGGCACCTACAAATGCCATCATTGCCGATAAAGGCCATCGTTCAAGATGCC 531
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Db   388 GAAGGTGGCCTCTACAAATGCCATCATTGCCGATAAAGGCCATCGTTGAAGATGCC 447

Qy   532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCACCCACCCACGAGGAGCATCGTGGAAAAAGAA 591
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Db   448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCACCCACCCACGAGGAGCATCGTGGAAAAAGAA 507

Qy   592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 651
             ||| || |||||||||||||||| |||||||||||||||||||||||||||||||
Db   508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 567

Qy   652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTTCCTCTATATAAGGAAGTTCATTT 711
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Qy   712 CATTTGGAGGAGGACACGCTG 731
             |||||||||||||||||||||
Db   628 CATTTGGAGGAGGACACGCTG 647

Qy    652 GATGACGCAACATCCCACTATCCTTCGGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
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Db    548 GATGACGCAACATCCCACTATCCTCCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 607

Qy    712 CATTTGGAGAGGACAGGCTG 731
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Db    608 CATTTGGAGAGGACAGGCTG 627

RESULT 5
US-09-441-340-31

; Sequence 31, Application US/09441340
; Patent No. 6448476
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard P.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/09/441,340
; CURRENT FILING DATE: 1999-11-16
; EARLIER APPLICATION NUMBER: 60/108,763
; EARLIER FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 31
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:monocot
; OTHER INFORMATION: expression cassette comprising plant operable
; OTHER INFORMATION: promoter linked to an intron, a sequence coding
; OTHER INFORMATION: for an AMPA acetyltransferase, and a termination
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (670)..(1473)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1498)..(1725)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1726)..(2157)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (2172)..(2427)

US-09-441-340-31

Query Match          75.3%;  Score 554;  DB 3;  Length 2436;
Best Local Similarity  94.5%;  Pred. No. 2.9e-175;
Matches 586;  Conservative   0;  Mismatches  30;  Indels   4;  Gaps   1;

Qy    116 TCTGCAGTGAGACTTTCACAAAGGAGGTAATATCCGGGAAACCTTCCTCCGGATTCCATTGCC 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     28 TCCGATGTGAGACATTTCACAAAGGAGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 87

Qy    176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGAAGCGGACCTACTACAAATGCC 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     88 CAGCTATCTGTCACTTTATTCTGTGAAGATAGTGGAAAAGGAAGGTGGTCCTCCTACAAATCCC 147

Qy    236 ATCATTCGATAAAGAAAGCTATCGTTCAAGATGCCTCTCCCACACGTGGTCCCAAAG 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 ATCATTCGGATAAAGAAAGCCATCGTTCAAGATGCCTTCTCCCACACCACGGTCTTCA 207

Qy    296 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAGAAGAAGCTTCCACCAGGGTCTTCAA 355
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Db    208 ATGGACCCCCACCACGAGGAGCATCGTGGAAAAGAAGAAGCTTCCAACCACGGTCTTCA 267

Qy    356 AGCAAGTGGATTGCATGCAT----TCCAGTGAGACTTTCAACAAAGGGGTAATATCCGGGA 411
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RESULT 6
US-09-377-466B-23

; Sequence 23, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Improved Exp. Corn
; FILE REFERENCE: 38-21(15504) Cry3BB Insecticidal Protein in Plants
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcbl
; FEATURE:
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1241)..(3199)
; OTHER INFORMATION: Cry3bb1 variant 11231mv2
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3217)..(3450)
; OTHER INFORMATION: T-Ta.hsp17

US-09-377-466B-23

Query Match          75.3%;  Score 554;  DB 3;  Length 3469;
Best Local Similarity  94.5%;  Pred. No. 3.5e-175;
Matches 586;  Conservative   0;  Mismatches  30;  Indels   4;  Gaps   1;

Qy    116 TCTGCAGTGAGACTTTCAACAAAGGTAATATCGGGAAACCTTCCTCCGGATTCCATTGCC 175
          ||| |||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     28 TCCGATGTGAGACATTTCAACAAAGGGTAATATCCGGAAACCTCCGGATTCCATTGCC 87

Qy    176 CAGCTATCTGTCACTTCATCAAAAAGGACAGTAGAAAAGGAGCAGTAGAAAATGCC 235
          ...

Db    268 AGCAAGTGGATTGCATGCATGGTGATGTCCGGATGTGGAGAGACTTTTCAACAAAGGAGCACGTAATATCCGGA 327
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Qy    412 AACCTCCCGGATCCATTGCCCAGCTATCTCGTCACTTCATCAAAAAGGACAGTAGAAAAAG 471
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Db    328 AACCTCCCGGATCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAAG 387
Qy    472 GAAGTGGCACCTACAAAATGCCATCATTCGGATAAAGAAAGCTATCGTTCAAGATGCC 531
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Db    388 GAAGGTGGCTCCTACAAAATGCCATCATTCGGATAAAGAAAGCCATCGTTCAAGATGCC 447
Qy    532 TCTGCCGACAGTGGTCCCAAAGATGAACCCCCACCCACGAGGAGCATCGTGGAAAAAGA 591
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Db    448 TCTGCCGACACGTGGTCCCAAAGATGAACCCCCACCCACGAGGAGCATCGTGGAAAAAGA 507
Qy    592 GAGGTTCCAACCACGGTTCTTCAAACGCAAGTGGAGTTGCATGCATTGATGTGAATATCTCCAGTGAGACGTAAGG 651
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Db    508 GAGGTTCCAACCACGGTTCTTCAAACGCAAGTGGATGATGTGAATATCTCCACTGACGTAAGG 567
Qy    652 GATGACGCAACATCCCACTATCCTTCGGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
          ...
Db    568 GATGACGCAACATCCCACTATCCTTCGGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627
Qy    712 CATTTGGAGAGGACAGGCTG 731
          ||||||||||||||||||||
Db    628 CATTTGGAGAGGACAGGCTG 647

NAME/KEY: CDS
LOCATION: (1241)..(3199)
OTHER INFORMATION: Cry3Bb1 variant 11231mv2
FEATURE:
NAME/KEY: terminator
LOCATION: (3217)..(3450)
OTHER INFORMATION: T-Ta.hsp17
US-10-232-665-23

Query Match      75.3%;  Score 554;  DB 3;  Length 3469;
Best Local Similarity   94.5%;  Pred. No. 3.5e-175;
Matches  586;  Conservative  0;  Mismatches 30;  Indels  4;  Gaps  1;

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Qy   116 TCTGCAGTGCAGACTTTTCAACAAAGGTAATATCGGGAAAACCTTCCGGATTCCATTGCC 175
             |||||| ||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    28 TCCGATGTGAGACTTTTCAACAAAGGTAATATCCGGAAACCTCTCCGGATTCCATTGCC 87

Qy   176 CAGCTATCTGTCACTTCATCAAAAGGACTAGAAAAGGAAGGTGCACCTACAAATGCC 235
             |||||||||||||||| ||||||||  ||||||||||||||||||||||||||||||
Db    88 CAGCTATCTGTCACTTATTGTGAAGATAGTGAAAAGGAAGGTGGCTCCTACAAATGCC 147

Qy   236 ATCATTGCGATAAAGGAAGGGCATCGTTCAAGATGGCCTCTGCCGACAGTGTCCCAAAG 295
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAGGAAGGGCATCGTTGAAGATGCCCTCTGCCGACAGTGTCCCAAAG 207

Qy   296 ATGGACCCCCACCAGGAGCAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208 ATGGACCCCCACCAGGAGCAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA 267

Qy   356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTCAACAAAGGGTAATATCGGGA 411
             |||||||||||||||||||       ||||||||||| ||||||||||||||||||||
Db   268 AGCAAGTGGATTGATGTGATGTCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGA 327

Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGACAGTAGAAAAG 471
             ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   328 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGGGTAATATCCGGA 387

Qy   472 GAAGGTGGCACCTACAAATGCCATCATTGCCGATAAAGGAAAGGCCATCGTTGAAGATGCC 531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   388 GAAGGTGGCTCCTACAAATGCCATCATTGCCGATAAAGGAAAGGCCATCGTTGAAGATGCC 447

Qy   532 TCTGCCGACAGTGGTCCCAAAGCAGTTCAAAGCAAGGTGGATTGATGTGAATCTCCACTGACGTAAGG 591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 TCTGCCGACAGTGGTCCCAAAGATGGACAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 507

Qy   592 GACGTTCCAACCAGTCTTCAAAGCAAGTGGATTGATGTGAATCTCCACTGACGTAAGG 651
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   508 GACGTTCCAACCAGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567

Qy   652 GATGAGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATAAGGAAGTTCATTT 711
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   568 GATGAGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATAAGGAAGTTCATTT 627

Qy   712 CATTTGGAGGAGGACACGCTG 731
             |||||||||||||||||||||
Db   628 CATTTGGAGGAGGACACGCTG 647
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RESULT 7
US-10-232-665-23
; Sequence 23, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/10/232,665
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US/09/377,466
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 3469
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (664)..(734)
; OTHER INFORMATION: L-Ta.hcb1
; FEATURE:
; NAME/KEY: intron
; LOCATION: (748)..(1238)
; OTHER INFORMATION: I-Os.Act1
; FEATURE:

RESULT 8
US-09-377-466B-15
; Sequence 15, Application US/09377466B
; Patent No. 6501009
; GENERAL INFORMATION:
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
; FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
; CURRENT APPLICATION NUMBER: US/09/377,466B
; CURRENT FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA

(Bottom-left, rotated alignment fragment:)
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Db    88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAGGGTAATATCCTCCTACAAATGCC 147
Qy   236 ATCATTGCGATAAAGGAAGGGCATCGTTCAAGATGCCTCTGCCGACAGTGTCCCAAAG 295
Db   148 ATCATTGCGATAAAGGAAGGGCATCGTTGAAGATGCCTCTGCCGACAGTGTCCCAAAG 207
Qy   296 ATGGACCCCCACCAGGAGCAGCATCGTGGAAAAAGAAGGACAGTAGAATATTCCGGA 355
Db   268 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
Qy   356 AGCAAGTGGATTGATGTGAT 411
Db   268 AGCAAGTGGATTGATGTGATGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327
Qy   412 AACCTCCTCGGATTCCAGCTATCGTCACTTCGTGCCATTGCCATCATTGCGATAAAGGAAAGA 471
Db   328 AACCTCCTCAACCACGTCTTCAAAGCAGTGGATTGATTGATATCTCCACTGGAAGAGATGAAAAGA 387
Qy   472 TCTGCCGACAGTGGTCCCAAAGCTTCAAAGCAAGCAAGTGATTGTGATTGTGATATCTTGAAGATGCC 531
Db   388 GAAGGTGGCTCCTACAAATGCCATCATTGCCATCATTGCCATCATTGCCATCATTGCCATCATTGCC 447
Qy   532 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 591
Db   448 GAAGGTGGCTCCTACAAATGCCATCATTGGCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC 507
Qy   592 TCTGCCGACAGTGGTCCCACCCACCTACTATCCTTCGGCAAGACCCTTCCTATATAAGGAAGTTCATTT 651
Db   508 GACGTTCCAACCAGTCCCACTATCCCACTATCCTTCGCAAGACCCTTCCTATATAAGGAAGTTCATTT 567
Qy   652 GATGACCCACAATCCCACTATCCTTCGGCAAGACCCTTCCTATATAAGGAAGTTCATTT 711
Db   568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTATATAAGGAAGTTCATTT 627
Qy   712 CATTTGGAGGAGGACACGCTG 731
Db   628 CATTTGGAGGAGGACACGCTG 647
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; NAME/KEY: CDS
; LOCATION: (1490)..(3448)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; NAME/KEY: terminator
; LOCATION: (3475)..(3730)
; OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
; OTHER INFORMATION: termination and polyadenylation sequence
US-09-377-466B-15

Query Match   75.3%;   Score 554;   DB 3;   Length 3754;
Best Local Similarity   94.5%;   Pred. No. 3.6e-175;
Matches 586;   Conservative   0;   Mismatches   30;   Indels   4;   Gaps   1;

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Qy  116 TCTCGAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
        ||| | |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCCGAAAACCTCCTCGGATTCCATTGCC 87

Qy  176 CAGCTATCGTCACTTCATCAAAAGGACAGTAGAAAGGACAAGTGGCACCTACAAATGCC 235
        ||| ||||||||||| || | || || |||| |||| || ||||| ||||||||||
Db   88 CAGCTATCGTCACTTTATTGTAGAGATAGTGGAAGGTAGTGGCTCCTACAAAATGCC 147

Qy  236 ATCATTGCCATAAAAGGAAAAGGCTATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 295
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 ATCATTGCCATAAAAGGAAAAGGCCATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 207

Qy  296 ATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAAGACGACGTTCCAACCACGTCTTCAA 355
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  208 ATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAAGACGACGTTCCAACCACGTCTTCAA 267

Qy  356 AGCAAGTGGATTGATGTGGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
        |||||||||||||||| |         |||||||||||||||||||||||||||||||| ||
Db  268 AGCAAGTGGATTGATGTGGATGTGTAATTGCAGTGAGACTTTTCAACAAAGGGTAATATCCCGA 327

Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGGACAGTAGAAAG 471
        |||||||||||||||||||||||||||||||||||| || | || || |||| |
Db  328 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTAGAGATAGTGGAAAG 387

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGCCATAAAAGGAAAAGGCTATCGTTCAAGATGCC 531
        ||||||||| |||||| ||||||||||||||||||||||||||||| |||||||||||||
Db  388 GAAGGTGGCTCCTACAAAATGCCATCATTGCCATAAAAGGAAAAGGCCATCGTTCAAGATGCC 447

Qy  532 TCTCCCGACAGTGGTCCCAAAGATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAA 591
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 TCTCGCCGACAGTGGTCCCAAAGATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAA 507

Qy  592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGGAT 651
        |||||||||||||||||||||||||||||||||||||||||||
Db  508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGGAT 567

Qy  652 GATGACGCGCAATCCACTACCTTCGCAAGACCCTTCCTCTCTATAAGAAGGAAGTTCATTT 711
        |||||| | ||| ||| || ||  | ||  ||| |  ||| || | || ||
Db  568 GATGACGCACAATCCCACTACCTTCGCAAGACCCTTCCTCTATAAGAAGGAAGTTCATTT 627

Qy  712 CATTTGGAGAGGAGACACGGCTG 731
        ||||||||||||||||||||||
Db  628 CATTTGGAGAGGAGACACGGCTG 647
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; RESULT 9
; US-10-232-665-15
; Sequence 15, Application US/10232665
; Patent No. 6943281
; GENERAL INFORMATION:

SEQ ID NO 15
; LENGTH: 3754
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: expression
; OTHER INFORMATION: cassette
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (25)..(640)
; OTHER INFORMATION: P-CaMV.35S
; FEATURE:
; NAME/KEY: intron
; LOCATION: (669)..(1472)
; OTHER INFORMATION: I-Zm.Hsp70
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1490)..(3448)
; OTHER INFORMATION: Cry3Bb1 variant v11231
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (3475)..(3730)
; OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
; OTHER INFORMATION: termination and polyadenylation sequence
US-10-232-665-15

Query Match   75.3%;   Score 554;   DB 3;   Length 3754;
Best Local Similarity   94.5%;   Pred. No. 3.6e-175;
Matches 586;   Conservative   0;   Mismatches   30;   Indels   4;   Gaps   1;

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Qy  116 TCTCGAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
        ||| | |||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCCGAAAACCTCCTCGGATTCCATTGCC 87

Qy  176 CAGCTATCGTCACTTCATCAAAAGGACAGTAGAAAGGACAAGTGGCACCTACAAATGCC 235
        ||| ||||||||||| || | || || |||| |||| || ||||| ||||||||||
Db   88 CAGCTATCGTCACTTTATTGTAGAGATAGTGGAAGGTAGTGGCTCCTACAAAATGCC 147

Qy  236 ATCATTGCCATAAAAGGAAAAGGCTATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 295
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 ATCATTGCCATAAAAGGAAAAGGCCATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 207

Qy  296 ATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAAGACGACGTTCCAACCACGTCTTCAA 355
        ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  208 ATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAAGACGACGTTCCAACCACGTCTTCAA 267

Qy  356 AGCAAGTGGATTGATGTGGAT-----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
        |||||||||||||||| |         |||||||||||||||||||||||||||||||| ||
Db  268 AGCAAGTGGATTGATGTGGATGTGTAATTGCAGTGAGACTTTTCAACAAAGGGTAATATCCCGA 327

Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGGACAGTAGAAAG 471
        |||||||||||||||||||||||||||||||||||| || | || || |||| |
Db  328 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTAGAGATAGTGGAAAG 387

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGCCATAAAAGGAAAAGGCTATCGTTCAAGATGCC 531
        ||||||||| |||||| ||||||||||||||||||||||||||||| |||||||||||||
Db  388 GAAGGTGGCTCCTACAAAATGCCATCATTGCCATAAAAGGAAAAGGCCATCGTTCAAGATGCC 447

Qy  532 TCTCCCGACAGTGGTCCCAAAGATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAA 591
        ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  448 TCTCGCCGACAGTGGTCCCAAAGATGGACCCCACCACCACGAGGAGCATCGTTGAAAAAGAA 507

Qy  592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGGAT 651
        |||||||||||||||||||||||||||||||||||||||||||
Db  508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGGAT 651
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Db  508 GAGGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567

Qy  652 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  568 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy  712 CATTTGGAGAGGACACGCTG 731
        ||||||||||||||||||||
Db  628 CATTTGGAGAGGACACGCTG 647

**RESULT 10**
US-09-182-117-1
; Sequence 1, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8012 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-1

Query Match    75.3%;  Score 554;  DB 3;  Length 8012;
Best Local Similarity  94.5%;  Pred. No. 5.4e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy  116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
        ||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 3044 TCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 3103

Qy  176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
        |||||||||||||| | ||||||||||||||||||||||||||||||||||||||||||
Db 3104 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGAGGTGGCCTCCACAAATGCC 3163

Qy  236 ATCATTGGGATAAAGGAAGGGCATCGGTCTCGCCGACAGTGGTCCCAAAG 295
        ||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3164 ATCATTGGGATAAAGGAAGGGCATCGTTGAAGATGCCTCCGCCGACAGTGGTCCCAAAG 3223

Qy  296 ATGGACCCCCCACCGAGGAGCATCGTGGAAAAAGAAGACGTTCAACCACGTTCAA 355
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3224 ATGGACCCCCCACCGAGGAGCATCGTGGAAAAAGAAGAGACGTTCAACCACGTCTTCA 3283

Qy  356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTCAACAAAGGGTAATATCGGGA 411
        ||||||||||||||||||||   || |||||||||||||||||||||||||||| ||
Db 3284 AGCAAGTGGATTGATGTGATGTCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGA 3343

Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
        |||||||||||||||||| | |||||||||||||| | ||||||||||||||||||||
Db 3344 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 3403

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGGGATAAAGGAAGGGCATCGTTCAAGATGCC 531
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3404 GAAGGTGGCCTCCACAAATGCCATCATTGGGATAAAGGAAGGGCATCGTTGAAGATGCC 3463

Qy  532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACCGAGGAGCATCGTGGAAAAAGAA 591
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Db 3464 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCGAGGAGCATCGTGGAAAAAGAA 3523

Qy  592 GAGGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 651
        ||||||||||||||||||||||||||||
Db 3524 GAGGTTCCAACCACGTCTTCAAAGCAAGCAAGTGGATTGATATCTCCACTGACGTAAGG 3583

Qy  652 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
        |||||||||||||||||||||
Db 3584 GATGACGGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 3643

Qy  712 CATTTGGAGAGGACACGCTG 731
        ||||||||||||||||||||
Db 3644 CATTTGGAGAGGACACGCTG 3663

**RESULT 11**
US-09-434-039A-1
; Sequence 1, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 8012
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-1

Query Match    75.3%;  Score 554;  DB 3;  Length 8012;
Best Local Similarity  94.5%;  Pred. No. 5.4e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy  116 TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
        ||| ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db 3044 TCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC 3103

Qy  176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
        |||||||||||||| | |||||||||||||||||||||||||||||
Db 3104 CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGAGGTGGCCTCCACAAATGCC 3163

Qy  236 ATCATTGGGATAAAGGAAGGGCATCGGTCTCGCCGACAGTGGTCCCAAAG 295
        ||||||||||||||||||||||||||||||||||||
Db 3164 ATCATTGGGATAAAGGAAGGGCATCGTTGAAGATGCCTCCGCCGACAGTGGTCCCAAAG 3223

Qy  296 ATGGACCCCCCACCGAGGAGCATCGTGGAAAAAGAAGACGTTCAACCACGTTCAA 355
        ||||||||||||||||||||||||||||||||||||||||||||||
Db 3224 ATGGACCCCCCACCGAGGAGCATCGTGGAAAAAGAAGAGACGTTCAACCACGTCTTCA 3283

Qy  356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTCAACAAAGGGTAATATCGGGA 411
        ||||||||||||||||||||   ||||||||||||||||||||||||||||| ||
Db 3284 AGCAAGTGGATTGATGTGATGTCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGA 3343

Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAG 471
        |||||||||||||||||||| ||||||||||||||| | |||||
Db 3344 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 3403

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGGGATAAAGGAAGGGCATCGTTCAAGATGCC 531
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db 3404 GAAGGTGGCCTCCACAAATGCCATCATTGCGGATAAAGGAAGGGCCATCGTTGAAGATGCC 3463

Qy  532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACCGAGGAGCATCGTGGAAAAAGAA 591
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RESULT 12
US-09-186-002-16
; Sequence 16, Application US/09186002B
; Patent No. 6489542
; GENERAL INFORMATION:
; APPLICANT: Corbin, David R.
; APPLICANT: Romano, Charles P.
; TITLE OF INVENTION: Improved Method for Transforming Plants to Express,
; TITLE OF INVENTION: delta-Endotoxins
; FILE REFERENCE: 38-21(13547) US Pat No. 6489542 09/186,002
; CURRENT APPLICATION NUMBER: US/09/186,0028
; CURRENT FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 8349
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3666)..(5573)
; OTHER INFORMATION: completely synthesized
US-09-186-002-16

Query Match             75.3%;  Score 554;  DB 3;  Length 8349;
Best Local Similarity   94.5%;  Pred. No. 5.6e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

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Qy     116 TCTGCAGTGAGACTTTTCAACAAAGGTAATAATCGGGAAAAACCTCCTCGGATTCCATTGCC 175
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Db    1807 TCCGATGAGACTTTTCAACAAAGGTTAATATCCGGAAACCTCCTCGGATTCCATTGCC 1866

Qy     176 CAGCTATCTGTCTCACTTTCATCAAAAGGACAGTAGAAAAAAGGACACTAGAAAATGCC 235
           ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    1867 CAGCTATCTGTCACTTTATTGTGTCAAGATGGCTCTCGGCGACGTGGCTCCTACAAATGCC 1926

Qy     236 ATCATTGCGATAAAGGAGAAAGGCTATCGTTCAAGATGCCTCTCGCCGACGTGGTCCCAAAG 295
           ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1927 ATCATTGCGATAAAGGAGAAAGGCCATCGTGTTGAAGATGCCTCTCCGACGTGGTCCCAAAG 1986

Qy     296 ATGGACCCCCACCCACCAGAGAGGCATCGTGGAAAAAGAAGAGAGCGTTCCAACCACGTTCCA 355
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Qy     412 AACCTCCTCGGATTCCATTGCCCAGCTACTCGTCACTTCATCAAAAGGACACTAGAAAATG 471
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Qy     472 GAAGGTGGCACCTACAATGCCATACTATTGGCGATAAAGGAGAAGGCTATCGTTCAAGATGCC 531
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Db    2167 GAAGGTGGCACCTACAATGCCATCATTGCGGATAAAGGAGAAGGCATCGTGTGGAAAGATGCC 2226

Qy     532 TCTCGCCGACAGTGGTCCCACGAGCGAGCACGTCATGTCGTGGGAAAAAGA 591
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Db       (...)
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RESULT 13
US-09-182-117-5
; Sequence 5, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION NUMBER: US/09/182,117
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-5

Query Match             75.3%;  Score 554;  DB 3;  Length 8418;
Best Local Similarity   94.5%;  Pred. No. 5.6e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

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Qy     176 CAGCTATCTGTCTCACTTTCATCAAAAGGACAGTAGAAAAAAGGACACTAGAAAATGCC 235
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Qy     236 ATCATTGCGATAAAGGAGAAAGGCTATCGTTCAAGATGCCTCTCGCCGACGTGGTCCCAAAG 295
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Db    3083 ATCATTGCGATAAAGGAGAAAGGCCATCGTGTTGAAGATGCCTCTCCGACGTGGTCCCAAAG 3142

Qy     296 ATGGACCCCCACCCACCAGAGAGGCATGTGTGGAAAAAGAAGAGAGCGTTCCAACCACGTTCCA 355
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Qy     356 AGCAAGTGGATTGATGATGTGAT-----TGCAGTGAGACTTTTCAACAAAGGTTAATAATCGGGGA 411
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Qy     472 GAAGGTGGCACCTACAATGCCATACTATTGGCGATAAAGGAGAAGGCTATCGTTCAAGATGCC 531
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Db    3323 AACCTCCTCGGATTCCAGCTATCTGTCACTTTATTGTGAGAGTGGGAAAG 3382
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Qy   592  GACGTTCAACCACGTCTTCAAAGCAAGTGGATTGATATCTCCACTGACGTAAGG  651
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Qy   712  CATTTGGAGAGGACACGCTG  731
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RESULT 15
US-09-182-117-4
; Sequence 4, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
;   APPLICANT:
;   TITLE OF INVENTION:  Transgenic Plant
;   NUMBER OF SEQUENCES:  27
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/09/182,117
;     FILING DATE:
;   CLASSIFICATION:
; INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  8798 base pairs
;     TYPE:  nucleic acid
;     STRANDEDNESS:  double
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  DNA (genomic)
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
US-09-182-117-4

Query Match           75.3%;  Score 554;  DB 3;  Length 8798;
Best Local Similarity 94.5%;  Pred. No. 5.7e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

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Db  3373  AGCAAGTGGATTGATTGTGATCGTTGAGACTTTTCAACAAAGGGTAATATCCGGA  3432
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RESULT 14
US-09-434-039A-5
; Sequence 5, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
;   APPLICANT:  MANNERLOEF, Marie
;   APPLICANT:  TERNING, Paul Peter
;   APPLICANT:  STEEN, Per
;   TITLE OF INVENTION:  Transgenic Plants
;   FILE REFERENCE:  09/434,039
;   CURRENT APPLICATION NUMBER:  US/09/434,039A
;   CURRENT FILING DATE:  1999-11-04
;   PRIOR APPLICATION NUMBER:  60/112,003
;   PRIOR FILING DATE:  1997-12-11
;   PRIOR APPLICATION NUMBER:  09/182,117
;   PRIOR FILING DATE:  1998-10-29
;   SOFTWARE:  PatentIn version 3.0
;   NUMBER OF SEQ ID NOS:  36
; SEQ ID NO 5
;   LENGTH:  8418
;   TYPE:  DNA
;   ORGANISM:  Sugar beet
US-09-434-039A-5

Query Match           75.3%;  Score 554;  DB 3;  Length 8418;
Best Local Similarity 94.5%;  Pred. No. 5.6e-175;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

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Db  3023  TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCTCGGATTCCATTGCC  3082
Qy   176  CAGCTATCTGTCACTTCATCATCAAAAGGACAGTAGAAAAGGAGGTGGCACCTACAAATGCC  235
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Db  3083  CAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAGATAGTGGAAGGTGGCCTCTACAAATGCC  3142
Qy   236  ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG  295
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Db  3143  ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG  3202
Qy   296  ATGGACCCCCACCCACGAGGAGCATCGTGAAAAAAGAAGACGTTCAACCACGTCTTCAA  355
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Db  3203  ATGGACCCCCACCCACGAGGAGCATCGTGAAAAAAGAAGACGTTCAACCACGTCTTCAA  3262
Qy   356  AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCCGGA  411
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Db  3263  AGCAAGTGGATTGATTGTGATCGTTGAGACTTTTCAACAAAGGGTAATATCCGGA  3322
Qy   412  AACCTCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCATCAAAAGGACAGTAGAAAAG  471
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Db  3323  AACCTCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG  3382
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Db  3553 TCTGCCGGACAGTGGTCCCAAAGATCGACCCCACCGAGGAGCATCGTCGGAAAAAAGAA 3612
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Db  3733 CATTTGGAGAGGAGACACGGCTG 3752
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Search completed: June  5, 2006, 05:16:24
Job time : 198 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:          June   5, 2006, 05:59:48 ; Search time 1299 Seconds
                 (without alignments)
                 6962.047 Million cell updates/sec

Title:          US-10-075-105C-1
Perfect score:  736
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters:        37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | % Query Match | Match Length | DB | ID | Description |
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| 1 | 736 | 100.0 | 736 | 10 | US-10-075-105C-1 | Sequence 1, Appli |
| 2 | 597.4 | 81.2 | 1360 | 10 | US-10-075-105C-3 | Sequence 3, Appli |
| 3 | 554 | 75.3 | 661 | 3 | US-09-943-692-33 | Sequence 33, Appl |
| 4 | 554 | 75.3 | 2107 | 6 | US-10-213-791-29 | Sequence 29, Appl |
| 5 | 554 | 75.3 | 2122 | 6 | US-10-213-791-25 | Sequence 25, Appl |
| 6 | 554 | 75.3 | 2436 | 6 | US-10-213-791-31 | Sequence 31, Appl |
| 7 | 554 | 75.3 | 2767 | 16 | US-11-186-196-1 | Sequence 1, Appli |
| 8 | 554 | 75.3 | 3469 | 6 | US-10-232-665-23 | Sequence 23, Appli |
| 9 | 554 | 75.3 | 3469 | 15 | US-11-192-801-23 | Sequence 23, Appl |
| 10 | 554 | 75.3 | 3754 | 6 | US-10-232-665-15 | Sequence 15, Appli |
| 11 | 554 | 75.3 | 3754 | 15 | US-11-192-801-15 | Sequence 15, Appl |
| 12 | 554 | 75.3 | 8349 | 7 | US-10-198-478-16 | Sequence 16, Appl |
| 13 | 551.4 | 74.9 | 5796 | 8 | US-10-759-602-26 | Sequence 26, Appl |
| 14 | 551.4 | 74.9 | 5897 | 8 | US-10-759-602-19 | Sequence 19, Appl |
| 15 | 550.4 | 74.8 | 9335 | 7 | US-10-198-478-14 | Sequence 14, Appl |
| 16 | 550 | 74.7 | 10249 | 7 | US-10-198-478-15 | Sequence 15, Appl |
| 17 | 550 | 74.7 | 10312 | 7 | US-10-198-478-15 | Sequence 15, Appl |

| 18 | 550 | 74.7 | 10339 | 7 | US-10-198-478-13 | Sequence 13, Appl |
| 19 | 548.4 | 74.5 | 10160 | 8 | US-10-759-602-8 | Sequence 8, Appli |
| 20 | 548.4 | 74.5 | 11784 | 8 | US-10-759-602-9 | Sequence 9, Appli |
| 21 | 548.4 | 74.5 | 11991 | 8 | US-10-759-602-10 | Sequence 10, Appl |
| 22 | 545.2 | 74.1 | 612 | 15 | US-11-038-981A-1 | Sequence 1, Appli |
| 23 | 543.6 | 73.9 | 4149 | 6 | US-10-232-665-13 | Sequence 13, Appl |
| 24 | 543.6 | 73.9 | 4149 | 15 | US-11-192-801-13 | Sequence 13, Appl |
| 25 | 534.6 | 72.6 | 5767 | 3 | US-09-810-861B-3 | Sequence 3, Appli |
| 26 | 534.6 | 72.6 | 5767 | 8 | US-10-792-491-3 | Sequence 3, Appli |
| 27 | 534.6 | 72.6 | 14446 | 3 | US-09-810-861B-4 | Sequence 4, Appli |
| 28 | 534.6 | 72.6 | 14446 | 8 | US-10-792-491-4 | Sequence 4, Appli |
| 29 | 526 | 71.5 | 829 | 6 | US-10-109-812-10 | Sequence 10, Appl |
| 30 | 526 | 71.5 | 1334 | 7 | US-10-322-656-12 | Sequence 12, Appl |
| 31 | 526 | 71.5 | 11478 | 10 | US-10-473-945-2 | Sequence 2, Appli |
| 32 | 526 | 71.5 | 12304 | 10 | US-10-473-945-5 | Sequence 5, Appli |
| 33 | 526 | 71.5 | 12497 | 10 | US-10-473-945-4 | Sequence 4, Appli |
| 34 | 514 | 69.8 | 8428 | 7 | US-10-161-403-90 | Sequence 90, Appl |
| 35 | 514 | 69.8 | 8428 | 9 | US-10-161-408-2 | Sequence 2, Appli |
| 36 | 514 | 69.8 | 8428 | 10 | US-10-161-408-2 | Sequence 90, Appl |
| 37 | 514 | 69.8 | 8428 | 13 | US-11-006-076-90 | Sequence 90, Appl |
| 38 | 514 | 69.8 | 8428 | 16 | US-11-082-154A-90 | Sequence 97, Appl |
| 39 | 514 | 69.8 | 10122 | 7 | US-10-161-403-97 | Sequence 97, Appl |
| 40 | 514 | 69.8 | 10122 | 9 | US-10-161-408-8 | Sequence 8, Appli |
| 41 | 514 | 69.8 | 10122 | 10 | US-10-161-408-8 | Sequence 8, Appli |
| 42 | 514 | 69.8 | 10122 | 13 | US-11-006-076-97 | Sequence 97, Appl |
| 43 | 514 | 69.8 | 10122 | 16 | US-11-082-154A-97 | Sequence 97, Appl |
| 44 | 514 | 69.8 | 10549 | 7 | US-10-161-403-92 | Sequence 92, Appl |
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## ALIGNMENTS

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RESULT 1
US-10-075-105C-1
; Sequence 1, Application US/10075105C
; Publication No. US2005018432A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhijian T
; APPLICANT: Gray, Dennis J
; TITLE OF INVENTION: Bi-Directional Dual Promoter Complex with Enhanced Promoter Acti
; TITLE OF INVENTION: Transgene Expression in Eukaryotes
; FILE REFERENCE: 7270-72978
; CURRENT APPLICATION NUMBER: US/10/075,105C
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 60/268,358
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 736
;   TYPE: DNA
;   ORGANISM: CaMV 35S
;   FEATURE:
;   OTHER INFORMATION:
US-10-075-105C-1

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  Matches  736;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db    241 TCCGATAAGGAAAGGCTATCGTTCAAGAAGATGCCTCTGCCGACAGTGGTCCCAAGATGGA 300

Qy    301 CCCCCACCCACGAGGAGCATGGTGGAAAAAGAGAGACGTTCCACACCAGGTCTTCAAAGCAA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 CCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGACGTTCCACACCAGGTCTTCAAAGCAA 360

Qy    361 GTGGGATTGATGTGATAGTCAGTGACACTTTCATCAAGAAGAGCAGACTTTCAACAAGAGCTCTC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 GTGGGATTGATGTGATATCAGTGACACTTTCATCAAGAAGAGCAGACTTTCAACAAGAGCTCTC 420

Qy    421 GGATTCCAGTCTATCGTCACTTCATCAAAAGGACTAGACAGTAGAAAAGGAAGGTGGC 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGATTCCAGTCTATCGTCACTTCATCAAAAGGACTAGACAGTAGAAAAGGAAGGTGGC 480

Qy    481 ACCTACAAAATGGCATCATTGCCATAAAAGGAAGGCTATCGTTCAAGATGTCCCTGCCGAC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ACCTACAAAATGGCATCATTGGCATAAAAGGAAGGCTATCGTTCAAGATGTCCCTGCCGAC 540

Qy    541 AGTGGTGTCCCAAAGATGGACCCCCCACCCACGAGGAGCATGGTGGAAAAAGAGAGACGTTCCA 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 AGTGGTGTCCCAAAGATGGACCCCCCACCCACGAGGAGCATCGTGGAAAAAGAGAGACGTTCCA 600

Qy    601 ACCAAGGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTCAGCTAAGGATGATGACGCA 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ACCAAGGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTCAGCTAAGGATGATGACGCA 660

Qy    661 CAATCCCACTATCCTTCGGCAAGACCCTTCCTTCTATATAAGGAAGTTCATTTGGAG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 CAATCCCACTATCCTTCGGCAAGACCCTTCCTTCTATATAAGGAAGTTCATTTGGAG 720

Qy    721 AGGACACGGTCGGATCC 736
          |||||||||||||||||
Db    721 AGGACACGGTCGGATCC 736
```

Query Match             81.2%;  Score 597.4;  DB 10;  Length 1360;
Best Local Similarity   99.8%;  Pred. No. 3.6e-191;
Matches  598;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

```
Qy    109 AGAAGCTTCTGCAGTGAGACTTTTCAACAAAAGGTAATATCGGGAAACCTCTCGGATTC 168
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    762 ATAAGCTTCTGCAGTGAGACTTTTCAACAAAAGGTAATATCGGGAAACCTCTCGGATTC 821
```

Query Match             75.3%;  Score 554;  DB 3;  Length 661;
Best Local Similarity   94.5%;  Pred. No. 1.3e-176;
Matches  586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

```
Qy    116 TCTCGAGTGAGACTTTTCAACAAAAGGTAATATCGGGAAACCTCTCGGATTCCATTGCC 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     20 TCCGGATGTGAGACTTTTCAACAAAAGGTAATATCGGGAAACCTCTCGGATTGCC 79

Qy    176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCC 235
          || || ||||||||||||||||||||||||| ||||| |||||| ||||| ||||||||||
Db     20 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCC 235
```

```
Db    80  CAGCTATCTGTCACTTTATTGTGTGAAGATAGTAGTGGAAAAGGAAGGTGGCTCCTACAAATGCC  139
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   236  ATCATTGCGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG  295
              ||||||||||||||||||||||||||||||||||||||||||||
Db   140  ATCATTGCGATAAAGGAAAGGCCATCGTTGCCGACAGTGGTCCCAAAG  199

Qy   296  ATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAGACGTTCCAACCACGTCTTCAA  355
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   200  ATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA  259

Qy   356  AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTCAACAAAGGGTAATATCGGGA  411
              |||||||||||||||||        ||||||||||||||||||||||||||||||
Db   260  AGCAAGTGGATTGATGTGGTTCCGATGTGAGACTTTCAACAAAGGGTAATATCGGGA  319

Qy   412  AACCTCCTCGGATTCCATTGCCCACTTCATGTCATCAAAAGGACTAGAAAAG  471
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   320  AACCTCCTCGGATTCCATTGCCCACGTCATCGTCACTTTATTGTGAAGATAGTGGAAAAG  379

Qy   472  GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGCTATCGTTCAAGATGCC  531
              |||||||||||||||||||||||||||||||||||||||||||||||
Db   380  GAAGGTGGCTCCTACAAATGCCATCATTGCCGATAAAGGCCATCGTTGAAGATGCC  439

Qy   532  TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAA  591
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   440  TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAA  499

Qy   592  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGAATGTGATATCTCCACTGACGTAAGG  651
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   500  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGAATGTGATATCTCCACTGACGTAAGG  559

Qy   652  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTT  711
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   560  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTT  619

Qy   712  CATTTGGAGAGGACACGCTG  731
              ||||||||||||||||||||
Db   620  CATTTGGAGAGGACACGCTG  639
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RESULT 4
US-10-213-791-29
; Sequence 29, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
;  APPLICANT: Barry, Gerard F.
;  TITLE OF INVENTION: Phosphonate Metabolizing Plants
;  FILE REFERENCE: 38-21(15303)
;  CURRENT APPLICATION NUMBER: US/10/213,791
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: US/09/441,340
;  PRIOR FILING DATE: 1999-11-16
;  PRIOR APPLICATION NUMBER: 60/108,763
;  PRIOR FILING DATE: 1998-11-17
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 29
;  LENGTH: 2107
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence:expression
;  OTHER INFORMATION: cassette comprising plant operable promoter linked
;  OTHER INFORMATION: to a leader, intron, a sequence encoding an AMPA
;  OTHER INFORMATION: acetyltransferase, and termination sequence
;  FEATURE:
;  NAME/KEY: promoter
;  LOCATION: (26)..(590)
;  FEATURE:
;  NAME/KEY: 5'UTR
;  LOCATION: (615)..(685)
;  FEATURE:
;  NAME/KEY: intron
;  LOCATION: (699)..(1148)

;  FEATURE:
;  NAME/KEY: transit peptide
;  LOCATION: (1149)..(1426)
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1427)..(1858)
;  FEATURE:
;  NAME/KEY: terminator
;  LOCATION: (1869)..(2102)
US-10-213-791-29

Query Match             75.3%;  Score 554;  DB 6;  Length 2107;
Best Local Similarity   94.5%;  Pred. No. 2.4e-176;
Matches  586;  Conservative   0;  Mismatches   30;  Indels    4;  Gaps    1;

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Qy   116  TCTGCAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC  175
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    28  TCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCC  87

Qy   176  CAGCTATCGTCACTCATCAAAAGACAGTAGAAAAGGACAGTGCACTCACAAAATGCC  235
              ||||||||||   || |||||||||||||||||||||||||
Db    88  CAGCTATCTGTCACTTTATTGTGAAGATAGTAGTGGAAAAGGAAGGTGGCTCCTACAAATGCC  147

Qy   236  ATCATTGCGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG  295
              ||||||||||||||||||||||||||||||||||||||||||||
Db   148  ATCATTGCGATAAAGGAAAGGCCATCGTTGCCGACAGTGGTCCCAAAG  207

Qy   296  ATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA  355
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   208  ATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAA  267

Qy   356  AGCAAGTGGATTGATGTGAT-----TGCAGTGAGACTTTCAACAAAGGGTAATATCGGA  411
              |||||||||||||||||        ||||||||||||||||||||||||||||
Db   268  AGCAAGTGGATTGATGTGATGTGCCGATGTGAGACTTTCAACAAAGGGTAATATCCGGA  327

Qy   412  AACCTCCTCGGATTCCATTGCCCAGTCATCGTCACTCGTCATCAAAAGACTAGAAAAG  471
              ||||||||||||||||||   || |||||||||||||||||||
Db   328  AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAAG  387

Qy   472  GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGCTATCGTTCAAGATGCC  531
              ||||| || |||||||||||||||||||||||||||||||
Db   388  GAAGGTGGCTCCTACAAATGCCATCATTGCCGATAAAGGCCATCGTTGAAGATGCC  447

Qy   532  TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAA  591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448  TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAA  507

Qy   592  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTATATCTCCACTGACGTAAGG  651
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   508  GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGTATATCTCCACTGACGTAAGG  567

Qy   652  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTT  711
              |||||||||||||||||||||||||||||||||||||||||||||||||
Db   568  GATGACGCACAATCCCACTATCCTTCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTT  627

Qy   712  CATTTGGAGAGGACACGCTG  731
              ||||||||||||||||||||
Db   628  CATTTGGAGAGGACACGCTG  647
```

RESULT 5
US-10-213-791-25
; Sequence 25, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
;  APPLICANT: Barry, Gerard F.
;  TITLE OF INVENTION: Phosphonate Metabolizing Plants
;  FILE REFERENCE: 38-21(15303)
;  CURRENT APPLICATION NUMBER: US/10/213,791
;  CURRENT FILING DATE:  2002-08-07
;  PRIOR APPLICATION NUMBER: US/09/441,340
;  PRIOR FILING DATE: 1999-11-16
;  PRIOR APPLICATION NUMBER: 60/108,763

; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 25
; LENGTH: 2122
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:expression
; OTHER INFORMATION: cassette comprising plant promoter linked to
; OTHER INFORMATION: sequence encoding AMPA acetyl transferase linked
; OTHER INFORMATION: to termination sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (6)..(620)
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (645)..(715)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (729)..(1178)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1179)..(1406)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1407)..(1838)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (1849)..(2082)
US-10-213-791-25

Query Match             75.3%;  Score 554;  DB 6;  Length 2122;
Best Local Similarity   94.5%;  Pred. No. 2.4e-176;
Matches 586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy  116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
            |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    8 TCCGATGCAGACTTTTCAACAAAGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 67

Qy  176 CAGCTATCGTGTCACTTCATCAAAAGGACAGTAGAAAAGGACAGTAGGACCTACAAAATGCC 235
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 CAGCTATCGTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTTCCTACACAAATGCC 127

Qy  236 ATCATTGCGATAAAGGAGAAAGGCATCTATCGTTCAAGATGCCTCTGCCGCACGTGGTCTCCCAAAG 295
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  128 ATCATTGCGATAAAGGAGAAAGGCCATTGTTGAAGATGCCTCTGCCGCACGTGGTCCCAAAG 187

Qy  296 ATGGAACCCCCACCCACGGAGAGGAGCATCGTTGGAGAAAGAAGACGGTTCCAACCACGTCTTCA 355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  188 ATGGAACCCCCACCCACGGAGAGGAGCATCGTTGGAGAAAGAAGACGGTTCCAACCACGTCTTCA 247

Qy  356 AGCAAGTGGATTGATGTGATGAT------TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
            |||||:|||||||||||||||||       |||||||||||||||||||||||||||||||||||
Db  248 AGCAAGTGGATTGATGTGGTCCGATGCAGACTTTTCAACAAAGGGTAATATCGGGA 307

Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTGTCACTTCTGTTCATCAAAAGACACTAGAAAAG 471
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  308 AACCTCCTCGGATTCCATTGCCCAGCTATCGTGTCACTTTATTGTGAAGATAGTGGAAAAG 367

Qy  472 GAAGGTGGCACTACAAAATCCCATCATCATTGCGGATAAAAGGAGGCTATCGTTCAAGATGCC 531
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  368 GAAGGTGGCTTCCTACACAAATGCCATCATTGCGATAAAAGGAGGCTATCGTTCAAGATGCC 427

Qy  532 TCTGCCGCACAGTGGTGGTCCCAAAGATGGAACCCCACCACCCACGGAGGAGGAGCATCGTTAAGG 591
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  428 TCTGCCGCACAGTGGTGGTCCCAAAGATGGAACCCCACCACCCACGGAGGAGGAGCATCGTTAAGG 487

Qy  592 GACGTTCCAACCACGTCTTCAAAGCAAGTGAATTGATTGATGTGATATCTCCACTGACGTAAGG 651
            ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  488 GACGTTCCAACCACGTCTTCAAAGCAAGTGAATTGATTGATGTGATATCTCCACTGACGTAAGG 547

Qy  652 GATGAGGCAGCAATCCCACTATCCTTCGCCAAGACCCTTCCTTCTATATAAGGAAGTTCATTT 711
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  608 CATTCGGAGGAGGACACGCTG 627

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Db  548 GATGAGGCAGCAATCCCACTATCCTTCGCCAAGACCCTTCCTTCTATATAAGGAAGTTCATTT 607
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  712 CATTCGGAGGAGGACACGCTG 731
            |||||||||||||||||||||
Db  608 CATTCGGAGGAGGACACGCTG 627

RESULT 6
US-10-213-791-31
; Sequence 31, Application US/10213791
; Publication No. US20030106096A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard P.
; TITLE OF INVENTION: Phosphonate Metabolizing Plants
; FILE REFERENCE: 38-21(15303)
; CURRENT APPLICATION NUMBER: US/10/213,791
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US/09/441,340
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/108,763
; PRIOR FILING DATE: 1998-11-17
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 31
; LENGTH: 2436
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:monocot
; OTHER INFORMATION: expression cassette comprising plant operable
; OTHER INFORMATION: promoter linked to an intron, a sequence coding
; OTHER INFORMATION: for an AMPA acetyltransferase, and a termination
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (26)..(640)
; FEATURE:
; NAME/KEY: intron
; LOCATION: (670)..(1473)
; FEATURE:
; NAME/KEY: transit_peptide
; LOCATION: (1498)..(1725)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1726)..(2157)
; FEATURE:
; NAME/KEY: terminator
; LOCATION: (2172)..(2427)
US-10-213-791-31

Query Match             75.3%;  Score 554;  DB 6;  Length 2436;
Best Local Similarity   94.5%;  Pred. No. 2.6e-176;
Matches 586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy  116 TCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
            |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   28 TCCGATGCAGACTTTTCAACAAAGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 87

Qy  176 CAGCTATCGTGTCACTTCATCAAAAGACAGTAGAAAAGGACAGTAGGACCTACAAAATGCC 235
            || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   88 CAGCTATCGTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTTCCTACACAAATGCC 147

Qy  236 ATCATTGCGATAAAGGAGAAAGGCATCTATCGTTCAAGATGCCTCTGCCGCACGTGGTCTCCCAAAG 295
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  148 ATCATTGCGATAAAGGAGAAAGGCCATTGTTGAAGATGCCTCTGCCGCACGTGGTCCCAAAG 207

Qy  296 ATGGAACCCCCACCCACGGAGAGGAGCATCGTTGGAGAAAGAAGACGGTTCCAACCACGTCTTCA 355
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  208 ATGGAACCCCCACCCACGGAGAGGAGCATCGTTGGAGAAAGAAGACGGTTCCAACCACGTCTTCA 267

Qy  356 AGCAAGTGGATTGATGTGATGAT------TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
            |||||:|||||||||||||||||       |||||||||||||||||||||||||||||||||||
Db  268 AGCAAGTGGATTGATGTGGTCCGATGCAGACTTTTCAACAAAGGGTAATATCGGGA 355

Db  268 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTCAACAAGGGTAATATCCGGA 327
        ||||||||||||||||||||||||||||||||||||||  ||  ||  |||||||||||
Qy  412 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTCATCAAAAGGACCAGTAGAAAAG 471
        |||||||||||||||||||||||||||| |||  || |  || |||||||
Db  328 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTATTGTGAAGATAGTGGAAAAG 387

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGCGGATAAAGGCTATCGTTCAAGATGCC 531
        |||||||  || || |||  || |||||||||||||||||||||
Db  388 GAAGGTGGCTCCTACAAATGCCATCATTGCGGATAAAGGCCATCGTTGAAGATGCC 447

Qy  532 TCTGCCGACAGTGGTCCCAAAGATGACCCCACCCACCGAGGACATCGTGAAAAAGAA 591
        ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db  448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCACCCACCGAGGACATCGTGAAAAAGAA 507

Qy  592 GACGTTCCAACCACGTCTTCAAAGCAAGTGATGTGATATCTCCACTGACGTAAGG 651
        |||||||||||||||||||||||||| || ||||| |||||||||||||||||||
Db  508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 567

Qy  652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 711
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  568 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy  712 CATTTGGAGAGGACACGCTG 731
        ||||||||||||||||||||
Db  628 CATTTGGAGAGGACACGCTG 647

RESULT 7
US-11-186-196-1
; Sequence 1, Application US/11186196
; Publication No. US2006002671A1
; GENERAL INFORMATION:
;    APPLICANT: Gilbertson, Larry A
;    APPLICANT: Huang, Shihshieh
;    TITLE OF INVENTION: Non-Systemic Gene Suppression in Plants
;    FILE REFERENCE: 38-21(53709)C
;    CURRENT APPLICATION NUMBER: US/11/186,196
;    CURRENT FILING DATE: 2005-07-20
;    PRIOR APPLICATION NUMBER: 60/589,643
;    PRIOR FILING DATE: 2004-07-21
;    NUMBER OF SEQ ID NOS: 1
;    SEQ ID NO 1
;    LENGTH: 2767
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic construct
US-11-186-196-1

Query Match     75.3%;  Score 554; DB 16; Length 2767;
Best Local Similarity   94.5%;  Pred. No. 2.8e-176;
Matches  586; Conservative  0; Mismatches  30; Indels  4; Gaps  1;

Qy  116 TCTGCAGTGAGACTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175
        || || ||||||||||||||||||||||||| |||  |||||||||||||||||||||
Db    3 TCCGATGTGAGACTTTCAACAAGGGTAATATCCGGATAAACCTCCTCGGATTCCATTGCC 62

Qy  176 CAGCTATCGTCACTTCATCAAAAGGACCAGTGAAAAAGGAAGGTGGCACCTACAAATGCC 235
        |||||||||||||  |  || ||||||||||| | ||  |||||||||||| || |||||
Db   63 CAGCTATCGTCACTTATTGTGAAGATAGTGGAAAAAGGAAGGTGGCTCCTACAAATGCC 122

Qy  236 ATCATTGCGGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAG 295
        |||||||||||||||||||  ||||  |||| |||||||||||||||||||||||||
Db  123 ATCATTGCGGATAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAG 182

Qy  296 ATGGACCCCACCCACCGAGGACATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAA 355
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  183 ATGGACCCCACCCACCGAGGACATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAA 242

Qy  356 AGCAAGTGGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
        ||||||||||||||||||||        |  |||||||  |||||||||||||||||||
Db  243 AGCAAGTGGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 302

RESULT 8
US-10-232-665-23
; Sequence 23, Application US/10232665
; Publication No. US20030115630A1
; GENERAL INFORMATION:
;    APPLICANT: Romano, Charles P.
;    TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;    FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;    CURRENT APPLICATION NUMBER: US/10/232,665
;    CURRENT FILING DATE: 2002-08-29
;    PRIOR APPLICATION NUMBER: US/09/377,466
;    PRIOR FILING DATE: 1999-08-19
;    NUMBER OF SEQ ID NOS: 43
;    SOFTWARE: Patentin Ver. 2.0
;    SEQ ID NO 23
;    LENGTH: 3469
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: expression
;    OTHER INFORMATION: cassette
;    FEATURE:
;    NAME/KEY: promoter
;    LOCATION: (25)..(640)
;    OTHER INFORMATION: P-CaMV.35S
;    FEATURE:
;    NAME/KEY: 5'UTR
;    LOCATION: (641)..(734)
;    OTHER INFORMATION: L-Ta.hcb1
;    FEATURE:
;    NAME/KEY: intron
;    LOCATION: (748)..(1238)
;    OTHER INFORMATION: I-Os.Act1
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1241)..(3199)
;    OTHER INFORMATION: Cry3Bb1 variant 11231mv2
;    FEATURE:
;    NAME/KEY: terminator
;    LOCATION: (3217)..(3450)
;    OTHER INFORMATION: T-Ta.hsp17
US-10-232-665-23

Query Match     75.3%;  Score 554; DB 6; Length 3469;
Best Local Similarity   94.5%;  Pred. No. 3.1e-176;
Matches  586; Conservative  0; Mismatches  30; Indels  4; Gaps  1;

Qy  116 TCTGCAGTGAGACTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCC 175

RESULT 9
US-11-192-801-23
Sequence 23, Application US/11192801
Publication No. US20050273802A1
GENERAL INFORMATION:
  APPLICANT: Romano, Charles P.
  TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
  FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
  CURRENT APPLICATION NUMBER: US/11/192,801
  CURRENT FILING DATE:  2005-07-29
  PRIOR APPLICATION NUMBER: US/10/232,665
  PRIOR FILING DATE:  2002-08-29
  PRIOR APPLICATION NUMBER: US/09/377,466
  PRIOR FILING DATE:  1999-08-19
  NUMBER OF SEQ ID NOS: 43
  SOFTWARE: Patentin Ver. 2.0

  SEQ ID NO 23
  LENGTH: 3469
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: expression
  FEATURE:
  NAME/KEY: promoter
  LOCATION: (25)..(640)
  OTHER INFORMATION: P-CaMV.35S
  FEATURE:
  NAME/KEY: 5'UTR

  FEATURE:
  OTHER INFORMATION: Description of Artificial Sequence: cassette
  FEATURE:
  NAME/KEY: promoter
  LOCATION: (748)..(1238)
  OTHER INFORMATION: I-Os.Act1
  FEATURE:
  NAME/KEY: intron
  LOCATION: (748)..(1238)
  OTHER INFORMATION: I-Os.Act1
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1241)..(3199)
  OTHER INFORMATION: Cry3Bb1 variant 11231mv2
  FEATURE:
  NAME/KEY: terminator
  LOCATION: (3217)..(3450)
  OTHER INFORMATION: T-Ta.hsp17
  US-11-192-801-23

  LOCATION: (664)..(734)
  OTHER INFORMATION: L-Ta.hcb1

Query Match     75.3%;  Score 554;  DB 15;  Length 3469;
Best Local Similarity   94.5%;  Pred. No. 3.1e-176;
Matches  586;  Conservative   0;  Mismatches  30;  Indels   4;  Gaps   1;

Qy    116 TCTGCAGTGAGACTTTCAACAAAGGTAATATCGGGAAAACCTTCCATTGGAA 175
          |||||||| ||||||||||||||||||||||||||||||| |||||||||||||||
Db     28 TCCGAGTGAGAGACTTTTCAACAAAAGGTAATAATCCGGGAAAACCTTCCATTGGCC 87

Qy    176 CAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGTGGCACCTACAAAATGCC 235
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     88 CAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAAGGAAGGTGGCTCCTACAAAATGCC 147

Qy    236 ATCATTGGGATAAAAGGAAAAGGCTTATCGTTCAACAAAGATAGTGGAA 295
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    148 GAAGGTGGCTCCTACAAAATGCCATCATTGGGATAAAAGGAAAAGGCTTATCGTTCAAAAATGCC 207

Qy    296 ATGGACCCCCAGCCCACGAGGAGCATCCTCGGAAAAGACGTTCCCAACCACGTCTTCAA 355
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    208 ATGGACCCCCAGCCCACGAGGAGCATCCTCGGGAAAAGACGTTCCCAACCACGTCTTCAA 267

Qy    356 AGCAAGTAGGATTGATTGTGAT------TGCAGTGAGACTTTCAACAAAGGTAATATCCGGGA 411
          ||||||||||||||||||||||      |||||||||||||||||||||||||||||||||||
Db    268 AGCAAGTGGATTGATTGTGGAAAAAAGACTTTTCAACAAAGGGTAATATCCGGA 327

Qy    412 AACCTCCTCGGATTCCATTGCCCACGCTATCGTCACTTTATTGTGGAAGATAGTGAAAAAG 471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    328 AACCTCCTCGGATTCCATTGCCCACGCTATCGTCACTTTATTGTGAAGATAGTGAAAAAG 387

Qy    472 GAAGGTGGCACCTACAAAATGCCATCATTGGGATAAAAGGACAGTAGAAAAAGGAAGGTGG 531
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    388 GAAGGTGGCTCCTACAAAATGCCATCATTGGGATAAAAGGAAAAGGCCATGGTTAAGAATGCC 447

Qy    532 TCCTACAAAATGCCATCATTGGGATAAAAGGACAGTAGAAAAAGAA 591
          ||||||||||||||||||||||||||||||||||||||| |||||
Db    448 TCTGCGACGTGGTCCCCAAAGATGGATCGGATCCCCACCCGAGGAAAAGATGCCTTGGGGTCTCA 507

Qy    592 GACGTTCCAACCACGTCTCCAAAGATGGATTGAGTGGAATGATATCTCCACCTGACGTAAGG 651
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 GACGTTCCAACCACGTTCAAAGCGATAAGTGGATATATCTCCACTGACGTAAGG 567

Qy    652 GATGACGGCACAATCCCACTATCCTTCGGAAGCCACCTTCCTCTTATATAAGGAAGTTCATTT 711
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    568 GATGACGGCACAATCCCACTATCCTTCGGAAGACCCTTCCTCTATATAAGGAAGTTCATTT 627

Qy    712 CATTTCGGAGAGGACACGGCTG 731
          ||||||||||||||||||||||
Db    628 CATTTCGGAGAGGACACGGCTG 647

RESULT 10
US-10-232-665-15
Sequence 15, Application US/10232665
Publication No. US20030115630A1
GENERAL INFORMATION:
  APPLICANT: Romano, Charles P.
  TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
  FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn

CURRENT APPLICATION NUMBER: US/10/232,665
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US/09/377,466
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
    LENGTH: 3754
    TYPE: DNA
    ORGANISM: Artificial Sequence
    FEATURE:
    OTHER INFORMATION: Description of Artificial Sequence: expression
    OTHER INFORMATION: cassette
    FEATURE:
    NAME/KEY: promoter
    LOCATION: (25)..(640)
    OTHER INFORMATION: P-CaMV.35S
    FEATURE:
    NAME/KEY: intron
    LOCATION: (669)..(1472)
    OTHER INFORMATION: I-Zm.Hsp70
    FEATURE:
    NAME/KEY: CDS
    LOCATION: (1490)..(3448)
    OTHER INFORMATION: Cry3Bb1 variant v11231
    FEATURE:
    NAME/KEY: terminator
    LOCATION: (3475)..(3730)
    OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
    OTHER INFORMATION: termination and polyadenylation sequence
US-10-232-665-15

Query Match       75.3%;   Score 554;   DB 6;   Length 3754;
Best Local Similarity   94.5%;   Pred. No. 3.2e-176;
Matches 586;   Conservative  0;   Mismatches  30;   Indels  4;   Gaps   1;

Qy   116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGAAAACCTCCTCGGATTCCATTGCC 175
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCCGGAAACCTCCCGGATTCCATTGCC 87

Qy   176 CAGCTATCTGTCACTTCATCAAAAGGCAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
         |||||||||||| | | ||||||||| ||| | || |||||||||||||||||||||||
Db    88 CAGCTATCCGTCACTTATTGTGAAGATAGTGGAAAAGGAAGGTGCCTCCTACAAATGCC 147

Qy   236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 295
         |||||||||||| |||||||| |||||||||| |||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCGCCGACAGTGGTCCCAAAG 207

Qy   296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTTCAACCACGTCTTCAA 355
         |||||||||||||||| |||||||||| |||||||||||||| |||||||||||||||
Db   208 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTTCAACCACGTCTTCAA 267

Qy   356 AGCAAGTGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
         |||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db   268 AGCAAGTGATTGATGTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCCGA 327

Qy   412 AACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGCAGTAGAAAAG 471
         |||||||||||||||||||||||||||||||||||||||||||||| | ||||| | |||
Db   328 AACCTCCCGGATTCCATTGCCCAGCTATCCGTCACTTATTGTGAAGATAGTGGAAAAG 387

Qy   472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
         ||||||||||||||||||||||||||||||||||||||||||||  |||||||| |||||
Db   388 GAAGGTGCCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC 447

Qy   532 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAA 591
         ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   448 TCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAA 507

Qy   592 GACGTTCAACCACGTCTTCAAAGCAAGCAAGTGATTGAATATCTTCCACTGACGTAAGG 651
         ||||||||||||||||||||||||||| ||||||||||| | |||||||||||||||||
Db   508 GACGTTCAACCACCGTCTTCAAAGCAAGCAAGTGATTGAATATCTTCCACTGACGTAAGG 567

Qy   652 GATGACGCACAATCCCACTATCCTTCGGCAAGACCCTTCCTCCTCTATATAAGGAAGTTCATTT 711
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   652 GATGACGCACAATCCCACTATCCTTCGGCAAGACCCTTCCTCCTCTATATAAGGAAGTTCATTT

Db   568 GATGACGCACAATCCCACTATCCTTCGGCAAGACCCTTCCTCCTCTATATAAGGAAGTTCATTT 627
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy   712 CATTTGGAGGAGACGGCTG 731
         |||||||||||||||||||
Db   628 CATTTGGAGGAGACGGCTG 647

RESULT 11
US-11-192-801-15
; Sequence 15, Application US/11192801
; Publication No. US2005027388A1
; GENERAL INFORMATION:
;   APPLICANT: Romano, Charles P.
;   TITLE OF INVENTION: Improved Expression of Cry3Bb Insecticidal Protein in Plants
;   FILE REFERENCE: 38-21(15304) Cry3Bb Improved Exp. Corn
;   CURRENT APPLICATION NUMBER: US/11/192,801
;   CURRENT FILING DATE: 2005-07-29
;   PRIOR APPLICATION NUMBER: US/10/232,665
;   PRIOR FILING DATE: 2002-08-29
;   PRIOR APPLICATION NUMBER: US/09/377,466
;   PRIOR FILING DATE: 1999-08-19
;   NUMBER OF SEQ ID NOS: 43
;   SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 3754
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: expression
;   OTHER INFORMATION: cassette
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (25)..(640)
;   OTHER INFORMATION: P-CaMV.35S
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: (669)..(1472)
;   OTHER INFORMATION: I-Zm.Hsp70
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1490)..(3448)
;   OTHER INFORMATION: Cry3Bb1 variant v11231
;   FEATURE:
;   NAME/KEY: terminator
;   LOCATION: (3475)..(3730)
;   OTHER INFORMATION: Agrobacterium tumefaciens nos 3' transcription
;   OTHER INFORMATION: termination and polyadenylation sequence
US-11-192-801-15

Query Match       75.3%;   Score 554;   DB 15;   Length 3754;
Best Local Similarity   94.5%;   Pred. No. 3.2e-176;
Matches 586;   Conservative  0;   Mismatches  30;   Indels  4;   Gaps   1;

Qy   116 TCTGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCC 175
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    28 TCCGATGTGAGACTTTTCAACAAAGGGTAATATCCCGGAAACCTCCCGGATTCCATTGCC 87

Qy   176 CAGCTATCTGTCACTTCATCAAAAGGCAGTAGAAAAGGAAGGTGGCACCTACAAATGCC 235
         |||||||||||| | | ||||||||| ||| | || ||||||||||||||||||||||||
Db    88 CAGCTATCCGTCACTTATTGTGAAGATAGTGGAAAAGGAAGGTGCCTCCTACAAATGCC 147

Qy   236 ATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCGCCGACAGTGGTCCCAAAG 295
         |||||||||||| |||||||| |||||||||| |||||||||||||||||||||||||
Db   148 ATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCGCCGACAGTGGTCCCAAAG 207

Qy   296 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTTCAACCACGTCTTCAA 355
         |||||||||||||||| |||||||||| |||||||||||||| |||||||||||||||
Db   208 ATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTTCAACCACGTCTTCAA 267

Qy   356 AGCAAGTGATTGATGTGAT----TGCAGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
         |||||||||||||||||||    |||||||||||||||||||||||||||||||||||
Db   268 AGCAAGTGATTGATTGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCCGGA 327

```
RESULT 12
US-10-198-478-16
;  Sequence 16, Application US/10198478
;  Publication No. US20030188336A1
;  GENERAL INFORMATION:
;   APPLICANT: Corbin, David R.
;   APPLICANT: Romano, Charles P.
;   TITLE OF INVENTION: Improved Methods for Transforming Plants to Express delta-Endotox
;   FILE REFERENCE: 38-21 (13547) B
;   CURRENT APPLICATION NUMBER: US/10/198,478
;   CURRENT FILING DATE: 2002-11-12
;   PRIOR APPLICATION NUMBER: 09/186, 002
;   PRIOR FILING DATE: 1998-11-04
;   NUMBER OF SEQ ID NOS: 18
;   SOFTWARE: Patentin version 3.1
;
;  SEQ ID NO 16
;   LENGTH: 8349
;   TYPE: DNA
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: completely synthesized
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(8349)
;   OTHER INFORMATION:
US-10-198-478-16

Query Match             75.3%;  Score 554;  DB 7;  Length 8349;
Best Local Similarity   94.5%;  Pred. No. 4.9e-176;
Matches  586;  Conservative   0;  Mismatches  30;  Indels  4;  Gaps  1;

Qy     412 AACCTCCCCGGATTCCATTGCCCAGCTATCTTCGTCACTTCATCAAAAGGACAGTAGAAAG 471
               ||||||||||||||||||||||||||||| |||||| |  | |||||| ||| |||||
Db     328 AACCTCCCCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 387

Qy     472 GAAGGTGGCACCTACAAAATGCCATCATTGGATACAGGAAAAGGCTATCGTTCAAGATGCC 531
               ||||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||
Db     388 GAAGGTGGCTCCTACAAAATGCCATCATTGGATACAGGAAAAGGCCATCGTTCAAGATGCC 447

Qy     532 TCTGCCGACAGTGGTGTCCCAAAGATGGACACCCCCACACCACAGGAGGAGCATCGTGGGA 591
               |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     448 TCTGCCGACAGTGGTGTCCCAAAGATGGACACCCCCACCACCACAGGAGCAGTCGTGGGA 507

Qy     592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATCGTCCCACTGACGTAAGG 651
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db     508 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATCGTCCCACTGACGTAAGG 567

Qy     652 GATGAGGACACAATCCCACTATCCTTCGGCAAGACCCTTCCTCTAATAAGGAAGTTCATTT 711
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     568 GATGAGGACAATCCCACTATCCTTCGGCAAGACCCTTCCTCTAATAAGGAAGTTCATTT 627

Qy     712 CATTTGGAGGAGGACACGCTG 731
               |||||||||||||||||||||
Db     628 CATTTGGAGGAGGACACGCTG 647
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RESULT 13
US-10-378-810-2/c
;  Sequence 2, Application US/10378810
;  Publication No. US20030213009A1
;  GENERAL INFORMATION:
;   APPLICANT: Rubin-Wilson, Beth
;   APPLICANT: Smith, Kelley A
;   TITLE OF INVENTION: PROMOTER AND INTRON FROM MAIZE ACTIN DEPOLYMERIZING
;   TITLE OF INVENTION: FACTOR
;   FILE REFERENCE: 50695
;   CURRENT APPLICATION NUMBER: US/10/378,810
;   CURRENT FILING DATE: 2003-03-04
;   PRIOR APPLICATION NUMBER: US 60/167,111
;   PRIOR FILING DATE: 1999-11-23
;   NUMBER OF SEQ ID NOS: 2
;   SOFTWARE: Patentin Ver. 2.0
;
;  SEQ ID NO 2
;   LENGTH: 5796
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:pDAB305
US-10-378-810-2

Query Match             74.9%;  Score 551.4; DB 7;  Length 5796;
Best Local Similarity   93.2%;  Pred. No. 3.1e-175;
Matches  588;  Conservative   0;  Mismatches  41;  Indels  2;  Gaps  1;

Qy     356 AGCAAGTGGATTGATGTGAT------TGCACTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
               |||||||||||||||||||||      ||||||||||||||||||||||||||||||||||
Db    2047 AGCAAGTGGATTGATGTGATGTCGATGGTCCGATGTGAGACTTTTCAACAAAGGGTAATATCGGGA 2106

Qy     412 AACCTCCCCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAG 471
               ||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db    2107 AACCTCCCCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAG 2166

Qy     472 GAAGGTGGCACCTACAAAATGCCATCATTGGATACAGGAAAAGGCTATCGTTCAAGATGCC 531
               ||||||||| |||||||||||||||||||||||||||||||||| |||||||||||||||
Db    2167 GAAGGTGGCTCCTACAAAATGCCATCATTGGATACAGGAAAAGGCCATCGTTCAAGATGCC 2226

Qy     532 TCTGCCGACAGTGGTGTCCCAAAGATGGACACCCCCACACCACAGGAGGAGCATCGTGGGA 591
               |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    2227 TCTGCCGACAGTGGTGTCCCAAAGATGGACACCCCCACCACCACAGGAGCAGTCGTGGGA 2286

Qy     592 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATCGTCCCACTGACGTAAGG 651
               ||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    2287 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATCGTCCCACTGACGTAAGG 2346

Qy     652 GATGAGGACACAATCCCACTATCCTTCGGCAAGACCCTTCCTCTAATAAGGAAGTTCATTT 711
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2347 GATGAGGACAATCCCACTATCCTTCGGCAAGACCCTTCCTCTAATAAGGAAGTTCATTT 2406

Qy     712 CATTTGGAGGAGGACACGCTG 731
               |||||||||||||||||||||
Db    2407 CATTTGGAGGAGGACACGCTG 2426
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                                                    MOLECULE TYPE: DNA
                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                              US-10-759-602-26

                                              Query Match     74.9%;  Score 551.4; DB 8;  Length 5897;
                                              Best Local Similarity  93.2%;  Pred. No. 3.1e-175;
                                              Matches  588;  Conservative  0; Mismatches  41; Indels  2; Gaps   1;

Qy   345 CACGTCTTCAAAGCAAGTGGATTGATGTGAT--TGCAGTGAGACTTTTCAACAAAGGGTA 402       Qy   105 CTGCGAAGCTTCTGCAGTGAGACTTTTCAACAAAGGTAATATCGGGAAACCCTCCTCGG 164
         ||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||              |||||    ||||||||||||||||||  | ||||||||||||||||||||||||||
Db  3310 CACGTCTTCAAAGCAAGTGGATTGATGTGATCGATGGAGACTTTTCAACAAAGGGTA 3251       Db    12 CTGCAGATCTGCATGGGTGGAGACTTTTCAACAAAGGGTAATATCCGGAAACCCTCTCGG  71

Qy   403 ATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCGTCATCATCAAAGGACA 462        Qy   165 ATTCCATTGCCCAGCTATCGTCACTTCATCAAATCAAAAGGACAGTAGAAAAGGAAGGTGGCAC 224
         |||||  ||||||||||||||||||||||||||||||||| ||| |  ||||||||              ||||||||||||||||||||||  |  |  |||||||||||||||||||||||||||
Db  3250 ATATCCGGAAACCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATA 3191       Db    72 ATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTAGTGAAAAGGAAGGTGGGTC 131

Qy   463 GTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAGTGCGATAAAGGAAAGGCTATCGTT 522       Qy   225 CTACAAATGCCATCATTGCGATAAAGGAAGGAAGGCTATCGTTCAAGATGCCTTCGCGACAG 284
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||              |||||||||||||  ||||||||||||| |  |   |||||| |  |||||||
Db  3190 GTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCAGTGCGATAAAGGAAAGGCCATCGTT 3131       Db   132 CTACAAATGCCATCATTGCGATAAAGGAAAGGAAAGGCATCGTTCGAAGATGCCTTCGCGACAG- 191

Qy   523 CAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTG 582       Qy   285 TGGTCCCAAAGATGACCCCCACCCACGAGGAGCATCGTTGGAAAAAGAGACGTTCCAAC 344
         |||||||||||||||||||||||||||||||||| ||||||||||||||||||||              |||||||||||||  | |  | ||||||||||||||  | |  | ||||||||||||
Db  3130 GAAGATGCCTCGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTG 3071       Db   192 TGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTTGGAAAAAGAGACGTTCCAAC 251

Qy   583 GAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 642       Qy   345 CACGTCTTCAAAGCAAGTGGATTGATGTGAT--TGCAGTGAGACTTTCACTCATCAAAAGGGTA 402
         ||||||||||||||||||||||||||||||||||  |||| ||||||||||||              |||||||||||||||||||||||||||||||  |  | |||||||||||||||| |
Db  3070 GAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 3011       Db   252 CACGTCTTCAAAGCAAGTGGATTGATGTGATCATCGATGGAGACTTTTCAACAAAGGGTA 311

Qy   643 GACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGA 702       Qy   403 ATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCGTCATCATCAAAAGGACA 462
         ||||||||||||||||||||||||||||||||||||||||||||||||||||              |||||  ||||||||||||||||||||||||| ||| |  |||||||||
Db  3010 GACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGA 2951       Db   312 ATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATA 371

Qy   703 AGTTCATTTCATTTGGAGAGGACACGCTGGA 733                                  Qy   463 GTAGAAAAGGAAGGTGCGCACCTACAAATGCCATCAGTGCGATAAAGGAAAGGCTATCGTT 522
         |||||||||||||||||||||||||||||                                          || |||||||||||||| ||||||||||||||||||||||  |||||||||||||
Db  2950 AGTTCATTTCATTTGGAGAGAACACGGGGGA 2920                                  Db   372 GTGGAAAGGAAGGTGGCTCCTACAAATGGCCATCATTGCGATAAAGGAAAGGCCATCGTT 431

                                                                             Qy   523 CAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTG 582
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                                                                             Db   432 GAAGATGCCTCGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTG 491

                                                                             Qy   583 GAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 642
                                                                                      |||||||||||||||||||||||  |||||||||||||||||||||||||||
                                                                             Db   492 GAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACT 551

                                                                             Qy   643 GACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGA 702
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;        STATE: Indiana
;        COUNTRY: USA
;        ZIP: 46268
;    COMPUTER READABLE FORM:
;        MEDIUM TYPE: Floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: Patentin Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/10/759,602
;        FILING DATE: 16-Jan-2004
;        CLASSIFICATION: <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;        NAME: Kraus, Eric J
;        CLASSIFICATION: <Unknown>
;    TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 317 337 5110
;        TELEFAX: 317 337 4847
;    INFORMATION FOR SEQ ID NO: 19:
;    SEQUENCE CHARACTERISTICS:
;        LENGTH: 9335 base pairs
;        TYPE: nucleic acid
;        STRANDEDNESS: double
;        TOPOLOGY: circular
;    MOLECULE TYPE: DNA
US-10-759-602-19
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Best Local Similarity  93.2%;  Pred No. 8.6e-175;
Matches 587;  Conservative  0;  Mismatches 41;  Indels  2;  Gaps  1;

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Qy       226 TACAAATGCCATCATTCCGATAAAAGGAAAGGCTATCGTTCAAGATGCCTCTCGCCACAGT 285
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Qy       464 TAGAAAAGGAAGGTGGCACCTACACTCACAAATGCCATCATTCCGATAAAAGGCTATCGTTC 523
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Qy       704 GTTCATTTCATTTGGAGGAGGACACGCTGGA 733
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Db      5452 GTTCATTTCATTTGGAGGAGGAACACGCGGGGA 5481
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          Copyright  GenCore version 5.1.9
          Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   June  5, 2006, 06:00:44 ; Search time 28 Seconds
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Perfect score:  736
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                Gapop 10.0 , Gapext 1.0

Searched :      246837 seqs, 58886990 residues

Total number of hits satisfying chosen parameters:     493674

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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## SUMMARIES

| Result No. | Score | % Query Match | Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|---|
| 1 | 554 | 75.3 | 6 | 5170 | 6 | US-10-525-318-11 | Sequence 11, Appl |
| 2 | 554 | 75.3 | 6 | 5600 | 6 | US-10-525-318-13 | Sequence 13, Appl |
| 3 | 505.2 | 68.6 | 7 | 7525 | 7 | US-11-248-986-29 | Sequence 29, Appl |
| 4 | 505.2 | 68.6 | 6 | 12125 | 6 | US-11-248-986-30 | Sequence 30, Appl |
| 5 | 342.6 | 46.5 | 8 | 8810 | 7 | US-11-258-704-40 | Sequence 40, Appl |
| 6 | 342.6 | 46.5 | 8 | 8819 | 7 | US-11-258-704-41 | Sequence 41, Appl |
| 7 | 279.6 | 38.0 | 6 | 6600 | 6 | US-10-525-318-5 | Sequence 5, Appl |
| 8 | 279.6 | 38.0 | 7 | 7000 | 6 | US-10-525-318-8 | Sequence 8, Appl |
| 9 | 253.4 | 34.4 | 6 | 2574 | 7 | US-11-248-986-31 | Sequence 31, Appl |
| 10 | 253.4 | 34.4 | 6 | 6889 | 7 | US-11-248-986-32 | Sequence 32, Appl |
| 11 | 242 | 32.9 | 6 | 266 | 6 | US-10-523-290-7 | Sequence 7, Appl |
| 12 | 242 | 32.9 | 6 | 508 | 6 | US-10-523-290-3 | Sequence 3, Appl |
| 13 | 99.2 | 13.5 | 6 | 5170 | 6 | US-10-525-318-11 | Sequence 11, Appl |
| 14 | 99.2 | 13.5 | 6 | 5600 | 6 | US-10-525-318-13 | Sequence 13, Appl |
| 15 | 98.8 | 13.4 | 7 | 8810 | 7 | US-11-258-704-40 | Sequence 40, Appl |
| 16 | 98.8 | 13.4 | 7 | 8819 | 7 | US-11-258-704-41 | Sequence 41, Appl |
| 17 | 96.4 | 13.1 | 7 | 7525 | 7 | US-11-248-986-29 | Sequence 29, Appl |
| 18 | 96.4 | 13.1 | 6 | 12125 | 6 | US-11-248-986-30 | Sequence 30, Appl |
| 19 | 85.4 | 11.6 | 6 | 6600 | 6 | US-10-525-318-5 | Sequence 5, Appl |
| 20 | 85.4 | 11.6 | 6 | 7000 | 6 | US-10-525-318-8 | Sequence 8, Appl |
| 21 | 49 | 6.7 | 6 | 266 | 6 | US-10-523-290-7 | Sequence 7, Appl |
| 22 | 49 | 6.7 | 6 | 508 | 6 | US-10-523-290-3 | Sequence 3, Appl |
| 23 | 32.8 | 4.5 | 6 | 612 | 7 | US-11-217-529-81202 | Sequence 81202, A |
| 24 | 31.2 | 4.2 | 3 | 516 | 7 | US-11-217-529-173886 | Sequence 173886, |
| 25 | 30.2 | 4.1 | 7 | 2880 | 7 | US-11-217-529-78074 | Sequence 78074, A |

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| 26 | | 29.8 | 4.0 | 3489 | 7 | US-11-106-014-93 | Sequence 93, Appl |
| 27 | | 29 | | 29 | 7 | US-10-953-349-22700 | Sequence 22700, A |
| 28 | c | 28.8 | 3.9 | 1394 | 6 | US-10-953-349-2577 | Sequence 2577, Ap |
| 28 | c | 28.8 | 3.9 | 1970 | 6 | US-11-121-154-44 | Sequence 44, Appl |
| 30 | c | 28.4 | 3.9 | 2601 | 7 | US-11-217-529-81965 | Sequence 81965, A |
| 31 | | 28.4 | 3.9 | 189 | 7 | US-11-301-554-944 | Sequence 944, App |
| 32 | | 28.4 | 3.9 | 359 | 7 | US-11-217-529-1369 | Sequence 1369, Ap |
| 33 | | 28.4 | 3.9 | 3663 | 7 | US-11-505-928-326 | Sequence 326, App |
| 34 | c | 28 | 3.8 | 10211 | 6 | US-11-293-697-810 | Sequence 810, App |
| 35 | | 28 | 3.8 | 2710 | 7 | US-10-953-349-19101 | Sequence 19101, A |
| 36 | c | 27.8 | 3.8 | 1320 | 6 | US-10-953-349-19101 | Sequence 19101, A |
| 37 | | 27.8 | 3.8 | 1320 | 6 | US-11-121-154-70 | Sequence 70, Appl |
| 38 | c | 27.8 | 3.8 | 2682 | 7 | US-11-504-120-5 | Sequence 5, Appl |
| 39 | | 27.8 | 3.8 | 5411 | 6 | US-10-504-120-6 | Sequence 6, Appli |
| 40 | | 27.6 | 3.8 | 561 | 6 | US-10-488-619-2256 | Sequence 2256, Ap |
| 41 | c | 27.6 | 3.8 | 1410 | 7 | US-11-217-529-3900 | Sequence 3900, Ap |
| 42 | c | 27.6 | 3.8 | 4305 | 7 | US-11-217-529-77088 | Sequence 77088, A |
| 43 | c | 27.4 | 3.7 | 1817 | 6 | US-10-953-349-19897 | Sequence 19897, A |
| 44 | | 27.4 | 3.7 | 1866 | 7 | US-11-217-529-75376 | Sequence 75376, A |
| 45 | | 27.2 | 3.7 | 2253 | 7 | US-11-217-529-80174 | Sequence 80174, A |

## ALIGNMENTS

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RESULT 1
US-10-525-318-11
; Sequence 11, Application US/10525318
; Publication No. US2006011244A1
; GENERAL INFORMATION:
;  APPLICANT: Monsanto Technology LLC
;  APPLICANT: Romano, Charles P
;  APPLICANT: Bogdanova, Natalia N
;  TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expre
;  TITLE OF INVENTION: Plants
;  FILE REFERENCE: 38-21(15414)
;  CURRENT APPLICATION NUMBER: US/10/525,318
;  CURRENT FILING DATE: 2005-02-23
;  PRIOR APPLICATION NUMBER: 60/407,428
;  PRIOR APPLICATION FILING DATE: 2002-08-29
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
;  LENGTH: 5170
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: fully synthetic expression cassette
;  FEATURE:
;  NAME/KEY: promoter
;  LOCATION: (26)..(640)
;  OTHER INFORMATION: P-e35S
;  FEATURE:
;  NAME/KEY: 5'UTL
;  LOCATION: (665)..(735)
;  OTHER INFORMATION: L-Ta.CAB
;  FEATURE:
;  NAME/KEY: Intron
;  LOCATION: (749)..(1239)
;  OTHER INFORMATION: I-Os.ACT1
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1241)..(4930)
;  OTHER INFORMATION: Cry1Bb variant
;  FEATURE:
;  NAME/KEY: transcription termination_sequence
;  LOCATION: (4931)..(4936)
;  OTHER INFORMATION: miscellaneous
;  FEATURE:
;  NAME/KEY: polyadenylation sequence
;  LOCATION: (4937)..(5170)
;  OTHER INFORMATION: T-Ta.hsp70
US-10-525-318-11
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FEATURE:
NAME/KEY: promoter
LOCATION: (26)..(640)
OTHER INFORMATION: P-e35S
FEATURE:
NAME/KEY: 5'UTL
LOCATION: (665)..(735)
OTHER INFORMATION: L-Ta.CAB
FEATURE:
NAME/KEY: Intron
LOCATION: (749)..(1239)
OTHER INFORMATION: I-Os.ACT1
FEATURE:
NAME/KEY: Transit peptide
LOCATION: (1255)..(1401)
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FEATURE:
NAME/KEY: Intron
LOCATION: (1402)..(1564)
OTHER INFORMATION: I-Zm.rbcs
FEATURE:
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OTHER INFORMATION: TP-Zm.rbcs
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LOCATION: (1652)..(5341)
OTHER INFORMATION: Cry1Bb variant
FEATURE:
NAME/KEY: transcription termination sequence
LOCATION: (5342)..(5347)
OTHER INFORMATION: miscellaneous
FEATURE:
NAME/KEY: polyadenylation sequence
LOCATION: (5350)..(5592)
OTHER INFORMATION: T-Os.LDH
US-10-525-318-13

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Best Local Similarity    94.5%;    Pred. No. 4e-173;
Matches 586;  Conservative  0;  Mismatches  30;  Indels  4;  Gaps  1;

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Qy  236  ATCATTGGATAAAAGGAAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAG  295
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; Publication No. US20060112448A1
; GENERAL INFORMATION:
;  APPLICANT: OSBOURN, ANNE E.
;  APPLICANT: QI, XIAOQUAN
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE: 2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Patentin version 3.3
; SEQ ID NO 29
;  LENGTH: 7525
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Maize recombinant DNA construct 1
US-11-248-986-29

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Best Local Similarity 86.7%;  Pred. No. 6.2e-157;
Matches 605; Conservative 0; Mismatches 8; Indels 85; Gaps 1;

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Db 5742 CTCCACTGACGTAAGGGATGAGCACAATCCACCTACCTATATCCTTCGGCCAAGACCCTTCCTCTAT 5801

Qy  696 ATAAGGAAGTTCATTTCATTTGGAGAGGACGAGCTGA 733
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Db 5802 ATAAGGAAGTTCATTTCATTTGGAGAGGACGAGCTGCA 5819

RESULT 4
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; Sequence 30, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:
;  APPLICANT: OSBOURN, ANNE E.
;  APPLICANT: QI, XIAOQUAN
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE: 2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Patentin version 3.3
; SEQ ID NO 30
;  LENGTH: 12125
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: maize recombinant DNA construct 2
US-11-248-986-30

Query Match           68.6%;  Score 505.2; DB 7;  Length 12125;
Best Local Similarity 86.7%;  Pred. No. 7.9e-157;
Matches 605; Conservative 0; Mismatches 8; Indels 85; Gaps 1;

Qy  121 AGTGAGACTTTCAACAAAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCCCAGCT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9742 ATTGAGACTTTCAACAAAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCCCAGCT 9801

Qy  181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACGTGGCACCTACAAATGCCATCAT 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9802 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGACGTGGCACCTACAAATGCCATCAT 9861

Qy  241 TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGCGACAGTGGTCTCCAAAGATGGA 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9862 TGCGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCGCGACAGTGGTCTCCAAAGATGGA 9921

Qy  301 CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCAACCACGTCTTCAAAGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 9922 CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCAACCACGTCTTCAAAGCAA 9981

Qy  361 GTGGATTGATGTGAT------------------------------------ 375
        |||||||||||||||
Db 9982 GTGGATTGATGTGATGCTTAGAAAATCCGTCAACATGGTGAGCACGACACTCCGTCTA 10041

Qy  376 ----------------------------TGCAGTGAGACTTTTCAACA 395
                                    |||||||||||||||||||
Db 10042 CTCCAAGAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCTATTGAGACTTTTCAACA 10101

Qy  396 AAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCCCAGCTACTTCGTCACTTCATCAA 455
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 10102 AAGGGTAATATCGGGAAAACCTCCTCGGATTCCATTGCCCAGCTACTTCGTCACTTCATCAA 10161

Qy  456 AAGGACAGTAGAAAAGGAAGGGAGGCTAGGCACCTACAAAATGCCATCATTGCGGATAAAGGAAAGGC 515

Qy 10162 AAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCATTGGATAAAAGGAAAAGGC 10221
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy 516 TATCGTTCAAGATGCCTTCGTCGCGACGTGGTCCTACAAATGCCATCATTGGATAAAAGGAAGGAG 575

Db 10222 TATCGTTCAAGATGCCTTCGTCGCGACGTGGTCCTACAAATGCCATCATTGGATAAAAGGAAGGAG 10281

Qy 576 CATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACACCAGTCTTCAACCAGTCGATTCAAGTCGATTAT 635
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 10282 CATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACACCAGTCTTCAACCAGTCGATTCAAGTCGATTAT 10341

Db 636 CTCCCACTGACGTAAGGATGAGATGAGCGGCAACAATCCCAACTATCCTTCCCGACGAGACCCTTCCTTCTAT 695

Db 10342 CTCCCACTGACGTAAGGATGAGACCACAATCCCAACTATCCTTCCGGCAGACCCTTCCTCTAT 10401

Qy 696 ATAAGGAAGTTCATTTCATTTGGAGGAGGACGACCTTCGA 735

Db 10402 ATAAGGAAGTTCATTTCATTTGGAGGAGGACGACCTTCGA 10439

---

RESULT 5
US-11-258-704-40/c

; Sequence 40, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Zhan-Bin
; APPLICANT: Stoop, Johan
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 40
; LENGTH: 8810
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH50

US-11-258-704-40

Query Match    46.5%;   Score 342.6; DB 7;   Length 8810;
Best Local Similarity   97.5%;   Pred. No. 3e-103;   Indels   0;   Gaps   0;
Matches   348;   Conservative   0;   Mismatches   9;   Indels   0;   Gaps   0;

Qy 379 AGTGAGACTTTTCAACAAAGGGTTAATATCCGGGAAAACCTCCTCGGATTCCATTCCCCAGCT 438
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4210 ATTGAGACTTTTCAACAAAGGATAATTTCCGGGAAAACCTCCTGGATTCCATTGCCCAGCT 4151

Qy 439 ATCTGTCACTTCATCAACAAAGGACAGTAGAAAAAGGAAGGAGGTGGGCACCTACAAATGCCATCAT 498
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4150 ATCTGTCACTTCATCGAACAAAGGACAGTAGAAAAGGAAGGAGGTGGGCACCTACAAATGCCATCAT 4091

Qy 499 TGGCGATAAAGGAAAAGGCGTATCGTTCAAGATGCCTTCGTCCCAAAGATGGA 558
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4090 TGGCGATAAAGGAAAAGGCTATCATCTTCAAGATGCCTTCGTCCCGACAGTGGTCCTACAAAGATGGA 4031

Qy 559 CCCCCACCACCAGACGAGGACATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACCAGTCAGTCTTCAAAGCAA 618
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4030 CCCCCACCACCAGACGAGGACATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACCAGTCAGTCTTCAAAGCAA 3971

Qy 619 GTGGATTGAGTGAGTATATTCCACTGAACTTGACGTAAGGGATGAGGCACAATCCCAACTATCCTTCG 678
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3970 GTGGATTGAGTGAGTATATTCCACTGACGTAAGGGGATGAGGCACAATCCCAACTATCCTTCG 3911

Qy 679 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGAGGACACGGCTGGATC 735
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 3910 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGAGGACACGGCTCGAGC 3854

---

RESULT 6
US-11-258-704-41/c

; Sequence 41, Application US/11258704
; Publication No. US20060101545A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Zhan-Bin
; APPLICANT: Stoop, Johan
; TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENE
; TITLE OF INVENTION: IN PLANTS
; FILE REFERENCE: BB-1551
; CURRENT APPLICATION NUMBER: US/11/258,704
; CURRENT FILING DATE: 2005-10-26
; PRIOR APPLICATION NUMBER: US 60/625,835
; PRIOR FILING DATE: 2004-11-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.3
;
; SEQ ID NO 41
; LENGTH: 8819
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid SH58

US-11-258-704-41

Query Match    46.5%;   Score 342.6; DB 7;   Length 8819;
Best Local Similarity   97.5%;   Pred. No. 3e-103;   Indels   0;   Gaps   0;
Matches   348;   Conservative   0;   Mismatches   9;   Indels   0;   Gaps   0;

Qy 379 AGTGAGACTTTTCAACAAAGGGTTAATATCCGGGAAAACCTCCTCGGATTCCATTCCCCAGCT 438
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5804 ATTGAGACTTTTCAACAAAGGATAATTTCCGGGAAAACCTCCTGGATTCCATTGCCCAGCT 5745

Qy 439 ATCTGTCACTTCATCAACAAAGGACAGTAGAAAAAGGAAGGAGGTGGGCACCTACAAATGCCATCAT 498
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5744 ATCTGTCACTTCATCGAACAAAGGACAGTAGAAAAGGAAGGAGGTGGGCACCTACAAATGCCATCAT 5685

Qy 499 TGGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTTCGTCCCGACAGTGGTCCTACAAAATGCCATCAT 558
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5684 TGGCGATAAAGGAAAAGGCTATCATTCAAGATGCCTTCGTCCCGACAGTGGTCCTACAAAGATGGA 5625

Qy 559 CCCCCACCACCAGACGAGGACATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACCAGTCAGTCTTCAAAGCAA 618
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5624 CCCCCACCACCAGACGAGGACATCGTGGAAAAAGGAAGAAGAGGACGGTTCCAACCAGTCAGTCTTCAAAGCAA 5565

Qy 619 GTGGATTGAGTGAGTATATTCCACTGACGTAAGGGATGAGGCACAATCCCAACTATCCTTCG 678
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5564 GTGGATTGAGTGAGTATATTCCACTGACGTAAGGGGATGAGGCACAATCCCAACTATCCTTCG 5505

Qy 679 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGAGGACACGGCTGGATC 735
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5504 CAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGAGGACACGGCTCGAGC 5448

---

RESULT 7
US-10-525-318-5

; Sequence 5, Application US/10525318
; Publication No. US20060112447A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P
; APPLICANT: Bogdanova, Natalia N
; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expr
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15414)
; CURRENT APPLICATION NUMBER: US/10/525,318
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/407,428
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 5
; LENGTH: 6600
; TYPE: DNA

APPLICANT: Bogdanova, Natalia N
TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expres
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15414)
CURRENT APPLICATION NUMBER: US/10/525,318
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 60/407,428
PRIOR FILING DATE: 2002-08-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1

SEQ ID NO 8
LENGTH: 7000
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fully synthetic expression cassette
FEATURE:
NAME/KEY: promoter
LOCATION: (174)..(490)
OTHER INFORMATION: P-CaMV 35S
FEATURE:
NAME/KEY: CDS
LOCATION: (526)..(1320)
OTHER INFORMATION: nptII
FEATURE:
NAME/KEY: transcription termination & polyadenylation sequence
LOCATION: (1325)..(1767)
OTHER INFORMATION: T-AGRtu.nos3'
FEATURE:
NAME/KEY: promoter
LOCATION: (1809)..(2386)
OTHER INFORMATION: P-FMV
FEATURE:
NAME/KEY: 5'UTL
LOCATION: (2407)..(2480)
OTHER INFORMATION: L-Os.betaTUB
FEATURE:
NAME/KEY: Intron
LOCATION: (2498)..(2614)
OTHER INFORMATION: I-Os.PAL
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (2644)..(2790)
OTHER INFORMATION: TP-Zm.rbcs
FEATURE:
NAME/KEY: Intron
LOCATION: (2791)..(2953)
OTHER INFORMATION: I-Zm.rbcs
FEATURE:
NAME/KEY: transit_peptide
LOCATION: (2954)..(3040)
OTHER INFORMATION: TP-Zm.rbcs
FEATURE:
NAME/KEY: CDS
LOCATION: (3041)..(6730)
OTHER INFORMATION: Cry1Bb variant
FEATURE:
NAME/KEY: transcription termination sequence
LOCATION: (6731)..(6736)
OTHER INFORMATION: miscellaneous sequence
FEATURE:
NAME/KEY: polyadenylation sequence
LOCATION: (6742)..(6981)
OTHER INFORMATION: T-Os.LDH

US-10-525-318-8

Query Match 38.0%; Score 279.6; DB 6; Length 7000;
Best Local Similarity 98.3%; Pred. No. 1.6e-82;
Matches 293; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 437 CTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCCATC 496
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 174 CTATCTGTCACTTCATCAAAAGGACAGTAGTAAAAGGAAGGTGGCACCTACAAAATGCCATC 233

---

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fully synthetic expression cassette
FEATURE:
NAME/KEY: promoter
LOCATION: (174)..(490)
OTHER INFORMATION: P-CaMV 35S
FEATURE:
NAME/KEY: CDS
LOCATION: (526)..(1320)
OTHER INFORMATION: nptII
FEATURE:
NAME/KEY: transcription termination & polyadenylation sequence
LOCATION: (1315)..(1767)
OTHER INFORMATION: T-AGRtu.nos3'
FEATURE:
NAME/KEY: transcription termination & polyadenylation sequence
LOCATION: (1325)..(1767)
OTHER INFORMATION: T-AGRtu.nos3'
FEATURE:
NAME/KEY: promoter
LOCATION: (1809)..(2386)
OTHER INFORMATION: P-FMV
FEATURE:
NAME/KEY: 5' untranslated leader
LOCATION: (2407)..(2480)
OTHER INFORMATION: L-Os.betaTubulin
FEATURE:
NAME/KEY: Intron
LOCATION: (2498)..(2614)
OTHER INFORMATION: I-Os.PAL
FEATURE:
NAME/KEY: CDS
LOCATION: (2644)..(6333)
OTHER INFORMATION: Cry1Bb variant
FEATURE:
NAME/KEY: transcription termination & polyadenylation sequence
LOCATION: (6345)..(6584)
OTHER INFORMATION: T-Os.LDH

US-10-525-318-5

Query Match 38.0%; Score 279.6; DB 6; Length 6600;
Best Local Similarity 98.3%; Pred. No. 1.6e-82;
Matches 293; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 437 CTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCCATC 496
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 174 CTATCTGTCACTTCATCAAAAGGACAGTAGTAAAAGGAAGGTGGCACCTACAAAATGCCATC 233

Qy 497 ATTGCGATAAAAGGAAAAGGCATCGTTCAAGATGCCTCTGCCGACAGTGTCCCAAAGATG 556
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 234 ATTGCGATAAAAGGAAAAGGCTATCATTCAAGATGCCTCTGCCGACAGTGTCCCAAAGATG 293

Qy 557 GACCCCCACCCACCCAGGAGGCATCGTGGAAAAAGAAGACGTTCAACCACGTCTTCAAAGC 616
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 294 GACCCCCACCCACCCAGGAGGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGC 353

Qy 617 AAGTGGATTGATGTGATATCTCCACTGACGTAAGCGG-ATGACGGCACAATCCCACTATCCT 675
        |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db 354 AAGTGGATTGATGTGATACTTCCCACTGACGTAAGCGAATGACGGCACAATCCCACTATCCT 413

Qy 676 TCGCAAGAGACCCTCCTCTATAATAAGGAAGTTCATTTGGAGAGGACACGCTGGA 733
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 414 TCGCAAGAGACCCTTCCTCTATAATAAGGAAGTTCATTTCATTTGGAGAGGACACGCTGGA 471

RESULT 8
US-10-525-318-8
; Sequence 8, Application US/10525318
; Publication No. US2006011244A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P

RESULT 9
US-11-248-986-31
; Sequence 31, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:
;  APPLICANT: QI, XIAOQUAN
;  APPLICANT: OSBOURN, ANNE E.
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE: 2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Patentin version 3.3
;  SEQ ID NO 31
;  LENGTH: 2574
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Soybean recombinant DNA construct 1

US-11-248-986-31

Query Match             34.4%;  Score 253.4;  DB 7;  Length 2574;
Best Local Similarity   99.6%;  Pred. No. 4.4e-74;
Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

```
Qy        497 ATTGGCGATAAAGGAAAGAAGGTATCGTTCAAGATGCCTTCTGCCGACAGTGGTCCCAAAGATG 556
              ||||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Db        234 ATTGGCGATAAAGGAAAGGGTATCATTCAAGATGCCTTCTGCCGACAGTGGTCCCAAAGATG 293

Qy        557 GACCCCCACCCACGGAGGAGCATCGTGGAAAAAGAAGAGACGTTCAACCACGTCTTCAAAGC 616
              |||||||||||||||||||||||||| |||||||||| |||||||||||||||||||||||
Db        294 GACCCCCACCCACGGAGGAGCATCGTGTGAAAAAGAGAGACGTTCAACCACGTCTTCAAAGC 353

Qy        617 AAGTGGATTGATGTGATGATATCTCCACGTAAGGG-ATAACGCACCACATCCCACTATCCT 675
              |||||||||||||||||  |  ||||||  ||| ||| | |||||||||||||||||||||
Db        354 AAGTGGATTGATGTGATTACTTCCACTGACCTGAAGGGAATGACCGCACCACATCCCACTATCCT 413

Qy        676 TCGGCAAGACCCTTCCCTATATAGGACACACTCGA 733
              || | |||||| |||||||||| |||||| |
Db        414 TCCCAAGACGCCTTCCCTATATAAGGACAGTTCATTTCATTGGGAGGAGGACACGGCTGAA 471
```

RESULT 10
US-11-248-986-32
; Sequence 32, Application US/11248986
; Publication No. US20060112448A1
; GENERAL INFORMATION:
;  APPLICANT: QI, XIAOQUAN
;  APPLICANT: OSBOURN, ANNE E.
;  TITLE OF INVENTION: ENZYMES INVOLVED IN TRITERPENE SYNTHESIS
;  FILE REFERENCE: BB1550 US NA
;  CURRENT APPLICATION NUMBER: US/11/248,986
;  CURRENT FILING DATE: 2005-10-12
;  PRIOR APPLICATION NUMBER: 60/619,203
;  PRIOR FILING DATE: 2004-10-15
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: Patentin version 3.3
;  SEQ ID NO 32
;  LENGTH: 6889
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Soybean Recombinant DNA construct 2

US-11-248-986-32

Query Match             34.4%;  Score 253.4;  DB 7;  Length 6889;
Best Local Similarity   99.6%;  Pred. No. 7.2e-74;
Matches  254;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

```
Qy        121 AGTGAGACTTTTCAACAAAAGGGTAATAATCGGGAAAACCTCCTCGGATTCCAATTGCCCAGCT 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 ATTGAGACTTTTCAACAAAAGGGTAATAATCGGGAAAACCTCCTCGGATTCCAATTGCCCAGCT 281

Qy        181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCCATCAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAAATGCCATCAT 341

Qy        241 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 TCGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 401

Qy        301 CCCCCACCCACGGAGGAGCATCGTGGAAAAAGAAGAGAGACGTTCCAACCACGTCTTCAAAGCAA 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 CCCCCACCCACGGAGGAGCATCGTGGAAAAAGAAGAGAGACGTTCCAACCACGTCTTCAAAGCA 461

Qy        361 GTGGATTGGATGTGAT 375
              ||||||||| ||||||
Db        462 GTGGATTGATGTGAT 476
```

RESULT 11
US-10-523-290-7/C
; Sequence 7, Application US/10523290
; Publication No. US20060095986A1
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Scott C.
;  APPLICANT: Cavato, Tracey A.
;  APPLICANT: Coombe, Timothy R.
;  TITLE OF INVENTION: CORN EVENT PV-ZMIR13 (MON863) PLANTS AND COMPOSITIONS AND METHO
;  TITLE OF INVENTION: DETECTION THEREOF
;  FILE REFERENCE: 38-21 (52221)B
;  CURRENT APPLICATION NUMBER: US/10/523,290
;  CURRENT FILING DATE: 2005-02-03
;  PRIOR APPLICATION NUMBER: 60/399,279
;  PRIOR FILING DATE: 2002-07-29
;  PRIOR APPLICATION NUMBER: PCT/US03/23860
;  PRIOR FILING DATE: 2003-07-23
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: Patentin version 3.1
;  SEQ ID NO 7
;  LENGTH: 266
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: 5' insert sequence
;  FEATURE:
;  NAME/KEY: DNA
;  LOCATION: (1)..(266)
;  OTHER INFORMATION: 5' insert sequence
US-10-523-290-7

Query Match             32.9%;  Score 242;  DB 6;  Length 266;

```
Best Local Similarity   96.1%;  Pred. No. 7.9e-71;
Matches 248; Conservative   0; Mismatches 10; Indels   0; Gaps   0;

Qy    427 CATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 CTTTCCGATCCTCACCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTAC 199

Qy    487 AAATGCCATCATTGCGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    198 AAATGCCATCATTGCGATAAAGGCTATCATTCAAGATGCCTCTGCCGACAGTGGT 139

Qy    547 CCCAAAGATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACG 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    138 CCCAAAGATGACCCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACG 79

Qy    607 TCTTCAAAGCAAGTGGATTGATGTGATATCTTCCACTGACGTAAGGGATGACGCACAATCC 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     78 TCTTCAAAGCAAGTGGATTGATGTGATACTTCCACTGACGTAAGGGATGACGCACAATCC 19

Qy    667 CACTATCCTTCGCAAGAC 684
          ||||||||||||||||||
Db     18 CACTATCCTTCGCAAGAC 1
```

RESULT 12
US-10-523-290-3/c
; Sequence 3, Application US/10523290
; Publication No.US2006005986A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Scott C.
; APPLICANT: Cavaco, Tracey A.
; APPLICANT: Coombe, Timothy R.
; TITLE OF INVENTION: CORN EVENT PV-ZMIR13 (MON863) PLANTS AND COMPOSITIONS AND METHODS
; TITLE OF INVENTION: DETECTION THEREOF
; FILE REFERENCE: 38-21 (52221)B
; CURRENT APPLICATION NUMBER: US/10/523,290
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: 60/399,279
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: PCT/US03/22860
; PRIOR FILING DATE: 2003-07-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 3
;   LENGTH: 508
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 5' genome + insert sequence
;   FEATURE:
;   NAME/KEY: DNA
;   LOCATION: (1)..(508)
;   OTHER INFORMATION: 5' genome + insert sequence
US-10-523-290-3

```
Query Match            32.9%;  Score 242; DB 6; Length 508;
Best Local Similarity   96.1%;  Pred. No. 1.1e-70;
Matches 248; Conservative   0; Mismatches 10; Indels   0; Gaps   0;

Qy    427 CATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTAC 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    258 CTTTCCGATCCTCACCTGTCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTAC 199

Qy    487 AAATGCCATCATTGCGATAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGT 546
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Db    198 AAATGCCATCATTGCGATAAAGGCTATCATTCAAGATGCCTCTGCCGACAGTGGT 139

Qy    547 CCCAAAGATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACG 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    607 TCTTCAAAGCAAGTGGATTGATGTGATATCTTCCACTGACGTAAGGGATGACGCACAATCC 666
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Db     78 TCTTCAAAGCAAGTGGATTGATGTGATACTTCCACTGACGTAAGGGATGACGCACAATCC 19

Qy    667 CACTATCCTTCGCAAGAC 684
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RESULT 13
US-10-525-318-11/c
; Sequence 11, Application US/10525318
; Publication No.US2006011244A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; APPLICANT: Romano, Charles P
; APPLICANT: Bogdanova, Natalia N
; TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expres
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15414)
; CURRENT APPLICATION NUMBER: US/10/525,318
; CURRENT FILING DATE: 2005-02-23
; PRIOR APPLICATION NUMBER: 60/407,428
; PRIOR FILING DATE: 2002-08-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
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; SEQ ID NO 11
;   LENGTH: 5170
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: fully synthetic expression cassette
;   FEATURE:
;   NAME/KEY: promoter
;   LOCATION: (26)..(640)
;   OTHER INFORMATION: P-e35S
;   FEATURE:
;   NAME/KEY: 5'UTL
;   LOCATION: (665)..(735)
;   OTHER INFORMATION: L-Ta.CAB
;   FEATURE:
;   NAME/KEY: Intron
;   LOCATION: (749)..(1239)
;   OTHER INFORMATION: I-Os.ACT1
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1241)..(4930)
;   OTHER INFORMATION: Cry1Bb variant
;   FEATURE:
;   NAME/KEY: transcription_termination_sequence
;   LOCATION: (4931)..(4936)
;   OTHER INFORMATION: miscellaneous
;   FEATURE:
;   NAME/KEY: polyadenylation sequence
;   LOCATION: (4937)..(5170)
;   OTHER INFORMATION: T-Ta.hsp70
US-10-525-318-11

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Query Match            13.5%;  Score 99.2; DB 6; Length 5170;
Best Local Similarity   97.1%;  Pred. No. 4.8e-23;
Matches 101; Conservative   0; Mismatches   3; Indels   0; Gaps   0;

Qy      6 CAGCGTGTCCCTCCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCGAAGGA 65
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Db    647 CAGCGTGTCCCTCCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCGAAGGA 588

Qy     66 TAGTGGGATTGTGCGTCATCCCTACGTCAGTGGAGATACTGCA 109
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Db    587 TAGTGGGATTGTGCGTCATCCCTTACGTCAGTGGAGATATCACA 544
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RESULT 14
US-10-525-318-13/c
; Sequence 13, Application US/10525318
; Publication No.US2006011244A1

GENERAL INFORMATION:
  APPLICANT: Monsanto Technology LLC
  APPLICANT: Romano, Charles P
  APPLICANT: Bogdanova, Natalia N
  TITLE OF INVENTION: Nucleotide Sequences Encoding Cry1Bb Proteins for Enhanced Expres
  TITLE OF INVENTION: Plants
  FILE REFERENCE: 38-21(15414)
  CURRENT APPLICATION NUMBER: US/10/525,318
  CURRENT FILING DATE: 2005-02-23
  PRIOR APPLICATION NUMBER: 60/407,428
  PRIOR FILING DATE: 2002-08-29
  NUMBER OF SEQ ID NOS: 14
  SOFTWARE: Patentin version 3.1

SEQ ID NO 13
  LENGTH: 5600
  TYPE: DNA
  ORGANISM: Artificial Sequence
  FEATURE:
  OTHER INFORMATION: fully synthetic expression cassette
  FEATURE:
  NAME/KEY: promoter
  LOCATION: (26)..(640)
  OTHER INFORMATION: P-e35S
  FEATURE:
  NAME/KEY: 5'UTL
  LOCATION: (665)..(735)
  OTHER INFORMATION: L-Ta.CAB
  FEATURE:
  NAME/KEY: Intron
  LOCATION: (749)..(1239)
  OTHER INFORMATION: I-Os.ACT1
  FEATURE:
  NAME/KEY: Transit_peptide
  LOCATION: (1255)..(101)
  OTHER INFORMATION: TP-Zm.rbcs
  FEATURE:
  NAME/KEY: CDS
  LOCATION: (1652)..(534)
  OTHER INFORMATION: Cry1Bb variant
  FEATURE:
  NAME/KEY: Intron
  LOCATION: (1402)..(1564)
  OTHER INFORMATION: I-Zm.rbcs
  FEATURE:
  NAME/KEY: transit_peptide
  LOCATION: (1565)..(1651)
  OTHER INFORMATION: TP-Zm.rbcs
  FEATURE:
  NAME/KEY: transcription termination sequence
  LOCATION: (5342)..(5347)
  OTHER INFORMATION: miscellaneous
  FEATURE:
  NAME/KEY: polyadenylation sequence
  LOCATION: (5550)..(5592)
  OTHER INFORMATION: T-Os.LDH

RESULT 15
US-11-258-704-40
; Sequence 40, Application US/11258704

Query Match        13.5%;  Score 99.2;  DB 6;  Length 5600;
Best Local Similarity   97.1%;  Pred. No. 5e-23;
Matches  101;  Conservative   0;  Mismatches   3;  Indels   0;  Gaps   0;

Qy      6 CAGGGTGTCCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCCAAGGA 65
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    647 CAGGGTGTCCTCCAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCCAAGGA 588

Qy     66 TAGTGGGATTGTGGCGTCATCCCTTAGTCAGTGGAGATACTGCA 109
          |||||||||||||||||||||||||||||||||||||||||||||
Db    587 TAGTGGGAATTGTGGCGTCATCCCTTAGTCAGTGGAGATATCACA 544

---

Publication No. US20060101545A1
GENERAL INFORMATION:
  APPLICANT: Liu, Zhan-Bin
  APPLICANT: Stoop, Johan
  TITLE OF INVENTION: PM29 AND LEA3 PROMOTERS AND USE IN EXPRESSION OF TRANSGENIC GENE
  TITLE OF INVENTION: IN PLANTS
  FILE REFERENCE: BB-1551
  CURRENT APPLICATION NUMBER: US/11/258,704
  CURRENT FILING DATE: 2005-10-26
  PRIOR APPLICATION NUMBER: US 60/625,835
  PRIOR FILING DATE: 2004-11-08
  NUMBER OF SEQ ID NOS: 41
  SOFTWARE: Patentin version 3.3

SEQ ID NO 40
  LENGTH: 8810
  TYPE: DNA
  ORGANISM: Artificial
  FEATURE:
  OTHER INFORMATION: plasmid SH50
US-11-258-704-40

Query Match        13.4%;  Score 98.8;  DB 7;  Length 8810;
Best Local Similarity   98.0%;  Pred. No. 8.5e-23;
Matches  100;  Conservative   0;  Mismatches   2;  Indels   0;  Gaps   0;

Qy      2 GATCCAGGGTGTCCTCCCAAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCCA 61
          | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3854 GCTCGAGGGTGTCCTCCCAAAATGAAATGAACTTCCTTATATAGAGGAAGGGTCTTGCCA 3913

Qy     62 AGGATAGTGGGAATTGTGGCGTCATCCCTTACGTCAGTGGGAGAT 103
          |||||||||||||||||||||||||||||||||||||||||||||
Db   3914 AGGATAGTGGGAATTGTGGCGTCATCCCTTACGTCAGTGGGAGAT 3955

Search completed: June  5, 2006, 06:01:22
Job time : 30 secs

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              GenCore version 5.1.9
       Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    June  5, 2006, 04:42:28 ; Search time 4658 Seconds
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Title:          US-10-075-105C-1
Perfect score:  736
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:   96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
         1:  gb_est1:*
         2:  gb_est3:*
         3:  gb_est4:*
         4:  gb_est5:*
         5:  gb_est6:*
         6:  gb_htc:*
         7:  gb_est2:*
         8:  gb_est7:*
         9:  gb_est8:*
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        11:  gb_gss1:*
        12:  gb_gss2:*
        13:  gb_gss3:*
        14:  gb_gss4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
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                              SUMMARIES

Result         %
No.    Score    Query    Match Length DB   ID          Description
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   2   546.6    74.3     702   8   CO472768   CO472768 GQ0081.BR
   3   546.6    74.3     755   8   CK438332   CK438332 GQ0083.BR
   4   546.6    74.3     803   8   CO472761   CO472761 GQ0081.BR
   5   544.6    74.0     713   5   CK437984   CK437984 GQ0081.BR
   6   544.6    74.0     741   5   CK438362   CK438362 GQ0083.BR
   7   537.2    73.0     655   5   CK437920   CK437920 GQ0081.BR
   8   535.2    72.7     736   5   CK438485   CK438485 GQ0085.BR
   9   533.2    72.4     698   5   CK438348   CK438348 GQ0085.BR
  10   480.8    65.3     610   8   CO481168   CO481168 GQ0165.B7
c 11   447.2    60.8     733   8   CX308688   CX308688 C21002G02
c 12   405      55.0     738   9   DN381521   DN381521 LIB38534_
c 13   354      48.1     685   9   DN381910   DN381910 LIB38534_
  14   351.8    47.8     839  11   AQ362115   AQ362115 mgAb0003F
c 15   344.4    46.8     869  13   CW799882   CW799882 WiscDsLox
  16   341      46.3     654  12   CG206846   CG206846 TOS0467 T
c 17   341      46.3     674   9   DN383492   DN383492 LIB38534_
c 18   339.4    46.1     761  13   CW800801   CW800801 WiscDsLox
c 19   334.2    45.4     496  12   CG730119   CG730119 11191I9Cl
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c  20  332.6  45.2   369  13   CZ909143   CZ909143   CZ909143 401800F0
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c  22  332.6  45.2   386  13   CZ909133   CZ909133   CZ909133 401800B0
c  23  332.6  45.2   467  12   BZ591291   BZ591291   BZ591291 3590_1_83
c  24  332.6  45.2   469  12   CG804983   CG804983   CG804983 1180056A0
c  25  332.6  45.2   490  12   BZ586494   BZ586494   BZ586494 3590_1_18
c  26  332.6  45.2   490  12   BZ588196   BZ588196   BZ588196 3590_1_6
c  27  332.6  45.2   524  12   BZ586946   BZ586946   BZ586946 3590_1_23
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c  29  332.6  45.2   528  12   CG805017   CG805017   CG805017 1180056D1
c  30  332.6  45.2   534  12   BZ586497   BZ586497   BZ586497 3590_1_18
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c  34  332.6  45.2   545  12   BZ590353   BZ590353   BZ590353 3590_1_76
c  35  332.6  45.2   549  12   BZ583905   BZ583905   BZ583905 3590_1_52
c  36  332.6  45.2   570  12   BZ586953   BZ586953   BZ586953 3590_1_23
c  37  332.6  45.2   572  11   BH618876   BH618876   BH618876 100025E1
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c  39  332.6  45.2   574  11   BH913058   BH913058   BH913058 3520_1_38
c  40  332.6  45.2   574  12   BZ587394   BZ587394   BZ587394 3520_1_13
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c  43  332.6  45.2   580  12   BZ586952   BZ586952   BZ586952 3590_1_23
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                           ALIGNMENTS

RESULT 1
CK438483
LOCUS       CK438483                 698 bp  mRNA     linear   EST 08-JAN-2004
DEFINITION  GQ0085.BR_M18 GQ008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GQ0085_M18 5', mRNA sequence.
ACCESSION   CK438483
VERSION     CK438483.1  GI:40769778
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1 (bases 1 to 698)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN id Identifier: MN5174605 Clone ID:
            GQ0085_M18 Clones available through: John MacKay, Ph. D. Professeur
            adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
            de Recherche en Biologie Forestiere (Forest Biology Research
            Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
            Plate: 5 row: 18 column: M
            Seq primer: M13 Reverse Primer.
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     source          1..698
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                     /mol_type="mRNA"
                     /strain="pg-653"
                     /db_xref="taxon:3330"
                     /clone="GQ0085_M18"
                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
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## Left column

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            from the midpoint of the main stem"
            /dev_stages="Vascular cambium; secondary phloem, and bark
            from trees harvested 1 and 7 days after girdling
            treatment"
            /lab_host="E. coli DH10B cells"
            /clone_lib="GO008: Cambium, phloem and bark of girdled
            saplings"
            /notes="Organ: Main stem of 4 year old saplings,
            approximately 60 cm tall; Vector; pBluescript II SK (+)
            XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
            from above and below the girdle. cDNA was prepared from 5
            mg of poly A+ selected RNA and was directionally ligated
            into the pBluescript II SK (+) XR vector (Stratagene),
            transformed by electroporation into DH10B cells (In
            vitrogen) for propagation"

ORIGIN
        Query Match     74.3%;  Score 546.6;  DB 5;  Length 698;
        Best Local Similarity   94.7%;  Pred. No. 2.7e-160;
        Matches 577;  Conservative  0;  Mismatches 29;  Indels  3;  Gaps  1;

Qy   121 AGTGAGACTTTTCAACAAAGGGTAATAATCGGGAAACCTTCCTCGGATTCCATTGCCCAGCT 180
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Db     4 ATTGAGACTTTTCAACAAAGGGTAATAATCCGGAAACCTTCCTCGGATTCCATTGCCCAGCT 63

Qy   181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGTGGCACTTACAAAATGCCATCAT 240
         ||||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db    64 ATCTGTCACTTTATTGTGAAGATAGTGAAAAAGGAAGGTGGCTTCCTACAGAATGCCATCAT 123

Qy   241 TGGGATAAAGGAAAGGCTATCCTTCAAGATGCCTTCTGCCCACAGTGGTCCCAAAGATGGA 300
         |||||||||||||||| |||| |||||||||| ||| |||||||||||||||||||||||
Db   124 TGGGATAAAGGAAAGGCCATCCGTGAAGATGCCTTCGCGCACAGTGGTCCCAAAGATGGA 183

Qy   301 CCCCCACCCAGGAGGAGCATCCTGGAAAAAAAGAAGAACGGTTCCAACCACGTCTTCAAAGCAA 360
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Db   184 CCCCCACCCAGGAGGAGCATCCGTGGAAAAAAGAAGAACGGTTCCAACCACGTCTTCAAAGCAA 243

Qy   361 GTTGGATTGATGTGATTG---CAGTGAGACTTTTCAACAAAGGGTAATATCGGGGAAACCTTC 417
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Qy   418 CTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGT 477
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Db   304 CTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAAGGAAGGT 363

Qy   478 GGGACTTACAAAATGCCATCATTGGGATAAAGGAAAGGCTTCCTACAGAATGCCTTCTGCC 537
         ||| ||||||||||||||||||||||||||||||||||| |||| ||||||||| ||||
Db   364 GGCTTCCTACAGAATGCCATCATTGGGATAAAGGAAAGGCCATCCGTGAAGATGCCTTCTGCC 423

Qy   538 GACAGTGGTCCCAAAGATGGACCCCCCACCCAGGAGGAGCATCGTGGAAAAAAGAACGTT 597
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Db   424 GACAGTGGTCCCAAAGATGGACCCCCACCCAGGAGGAGCATCCGTGGAAAAAAGAAGAACGTT 483

Qy   598 CCAACCACGTCTTCAAAGCAAGTTGGATTGATTGGATTGATGTGATATCTCCACTGACCTAAGGATGAC 657
         ||| |||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db   484 CCAACCACGTCTTCAAAGCAAGTGATTGATATCTCCACTGACGTAGGGATGAC 543

Qy   658 GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTG 717
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   544 GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTG 603

Qy   718 GAGAGGACA 726
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Db   604 GAGAGGAGA 612
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RESULT 2
LOCUS       CO472768        702 bp    mRNA    linear    EST 29-JUN-2005
DEFINITION  GO0081.BR.1.K09 GO008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GenomeQuebec_Id:GO0081K09 5', mRNA
            sequence.
ACCESSION   CO472768
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## Right column

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VERSION     CO472768.1  GI:50141325
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce).
ORGANISM    Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1 (bases 1 to 702)
AUTHORS     Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Scott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
TITLE       Arborea EST sequencing in Picea glauca (white spruce)
JOURNAL     Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN Id Identifier: MN5197113 Clone ID:
            GO0081.BR.K09 Clones available through: John MacKay, Ph. D.
            Professeur adjoint -Assistant professor EMAIL:
            jmackay@rsvs.ulaval.ca Centre de Recherche en Biologie Forestiere
            (Forest Biology Research Center) Universite Laval Quebec, Quebec
            CANADA G1K 7P4
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            Plate: 1.BR  row: 09  column: K
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                     /clone="GenomeQuebec_Id:GO0081K09"
                     /sex="Hermaphrodite"
                     /tissue_type="vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"
                     /dev_stage="Vascular cambium, secondary phloem, and bark
                     from trees harvested 1 and 7 days after girdling
                     treatment"
                     /lab_host="E. coli DH10B cells"
                     /clone_lib="GO008: Cambium, phloem and bark of girdled
                     saplings"
                     /notes="Organ: Main stem of 4 year old saplings,
                     approximately 60 cm tall; Vector; pBluescript II SK (+)
                     XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
                     from above and below the girdle. cDNA was prepared from 5
                     mg of poly A+ selected RNA and was directionally ligated
                     into the pBluescript II SK (+) XR vector (Stratagene),
                     transformed by electroporation into DH10B cells (In
                     vitrogen) for propagation"
ORIGIN
        Query Match     74.3%;  Score 546.6;  DB 8;  Length 702;
        Best Local Similarity   94.7%;  Pred. No. 2.7e-160;
        Matches 577;  Conservative  0;  Mismatches 29;  Indels  3;  Gaps  1;

Qy   121 AGTGAGACTTTTCAACAAAGGGTAATAATCGGGAAACCTTCCTCGGATTCCATTGCCCAGCT 180
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Db    29 ATTGAGACTTTTCAACAAAGGGTAATAATCCGGAAACCTTCCTCGGATTCCATTGCCCAGCT 88

Qy   181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGTGGCACTTACAAAATGCCATCAT 240
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Db    89 ATCTGTCACTTTATTGTGAAGATAGTGAAAAAGGAAGGTGGCTTCCTACAGAATGCCATCAT 148

Qy   241 TGGGATAAAGGAAAGGCTATCCTTCAAGATGCCTTCTGCCCACAGTGGTCCCAAAGATGGA 300
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Qy   301 CCCCCACCCAGGAGGAGCATCCTGGAAAAAAAGAAGAACGGTTCCAACCACGTCTTCAAAGCAA 360
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Db   209 CCCCCACCCAGGAGGAGCATCCGTGGAAAAAAGAAGAACGGTTCCAACCACGTCTTCAAAGCAA 268
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from the midpoint of the main stem"
/dev_stage="Vascular cambium, secondary phloem, and bark
from trees harvested 1 and 7 days after girdling
treatment"
/lab_host="E. coli DH10B cells"
/clone_lib="GQ008: Cambium, phloem and bark of girdled
saplings"
/note="Organ: Main stem of 4 year old saplings,
approximately 60 cm tall; Vector: pBluescript II SK (+)
XR; Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
from above and below the girdle. cDNA was prepared from 5
mg of poly A+ selected RNA and was directionally ligated
into the pBluescript II SK (+) XR vector (Stratagene),
transformed by electroporation into DH10B cells (in
vitrogen) for propagation"

ORIGIN

Query Match    74.3%;  Score 546.6;  DB 5;  Length 755;
Best Local Similarity  94.7%;  Pred. No. 2.7e-160;
Matches 577;  Conservative  0;  Mismatches 29;  Indels   3;  Gaps   1;

Qy    121  AGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT  180
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Db     32  ATTGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTCCGATTCCATTGCCCAGCT   91

Qy    181  ATCTGTCACTTCATCAAAGACAGTAGAAAAGGAAGGTGCACCTACAAATGCCATCAT   240
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Qy    241  TGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTCTGCCGACACAGTGGTCCCAAAGATGGA  300
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Db    152  TGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTCTGCCGCACAGTGGTCCCAAAGATGGA  211

Qy    301  CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA  360
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Db    212  CCCCACCCACGAGGAGCATCGTGGAAAAAGAAGAGACGTTCCAACCACGTCTTCAAAGCAA  271

Qy    361  GTGGATTGGATGTGATTG---CAGTGGAGACTTTCAACAAAGGGTAATATCGGGAAACCTC  417
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Db    272  GTGGATTGGATGTGATTGCCCAGTGGAGACTTTCAACAAAGGGTAATATCCGGAAACCTC  331

Qy    418  CTCGGATTCCATTGCCCAGCTATCGTCACTTCATCATCAAAGACAGTAGAAAAGGAAGGT  477
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Db    332  CTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGT  391

Qy    478  GGCACCTACAAATGCCATCATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC  537
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Db    392  GGCTCCTACAAATGCCATCATTGGGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC  451

Qy    538  GACAGTGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTT  597
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Db    452  GACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAGAAGACGTT  511

Qy    598  CCAACCACGTCTTCAAAGCAAGTGGATTGGATTGATGTGATAATCTCCACTGACGTAAGGCGATGAC  657
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Db    512  CCAACCACGTCTTCAAAGCAAGTGGATTGGATTGATGTGATAATCTCCACTGACGTAAGGGATGAC  571

Qy    658  GCAAATCCCACTATCCTTCGCCAAGACCCTCCTATATAAGGAAGTTCATTTCATTTG  717
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    572  GCAAATCCCACTATCCTTCGCCAAGACCCTCCTATATAAGGAAGTTCATTTCATTTG  631

Qy    718  GAGAGGACA 726
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Db    632  GAGAGGAGA 640

RESULT 4
CO472761
LOCUS        CO472761                  803 bp   mRNA     linear     EST 29-JUN-2005
DEFINITION   GQ0081.BR.1_G07 GQ008: Cambium, phloem and bark of girdled saplings
             Picea glauca cDNA clone GenomeQuebec_Id:GQ0081G07 5', mRNA
             sequence.
ACCESSION    CO472761

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Qy    361  GTGGATTGGATGTGATTG---CAGTGGAGACTTTCAACAAAGGGTAATATCGGGAAACCTC  417
           ||||||||||||||||||   |||| |||||||||||||||||||||||||||||||
Db    269  GTGGATTGGATGTGATTGCCCAGTGGAGACTTTCAACAAAGGGTAATATCCGGAAACCTC  328

Qy    418  CTCGGATTCCATTGCCCAGCTATCGTCACTTCATCATCAAAGACAGTAGAAAAGGAAGGT  477
           ||||||||||||||||||| |  ||| ||||||||||||||||||||||||||||||||
Db    329  CTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGT  388

Qy    478  GGCACCTACAAATGCCATCATTGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCC  537
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Db    389  GGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC  448

Qy    538  GACAGTGGTCCCAAAGATGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTT  597
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Qy    598  CCAACCACGTCTTCAAAGCAAGTGGATTGGATTGATGTGATAATCTCCACTGACGTAAGGGATGAC  657
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Db    509  CCAACCACGTCTTCAAAGCAAGTGGATTGGATTGATGTGATAATCTCCACTGACGTAAGGGATGAC  568

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Db    569  GCAAATCCCACTATCCTTCGGACGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTG  628

Qy    718  GAGAGGACA 726
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Db    629  GAGAGGAGA 637

RESULT 3
CK438332
LOCUS        CK438332                  755 bp   mRNA     linear     EST 29-JUN-2005
DEFINITION   GQ0083.BR_H02 GQ008: Cambium, phloem and bark of girdled saplings
             Picea glauca cDNA clone GenomeQuebec_Id:GQ0083H02 5', mRNA
             sequence.
ACCESSION    CK438332
VERSION      CK438332.1  GI:40769292
KEYWORDS     EST.
SOURCE       Picea glauca (white spruce)
ORGANISM     Picea glauca
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE    1  (bases 1 to 755)
AUTHORS      Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
             Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
             Siddiqui,A., Holt,R. Marra,M. and MacKay,J.
TITLE        Arborea EST sequencing in Picea glauca (white spruce)
JOURNAL      Unpublished (2004)
COMMENT      Contact: John MacKay
             Centre de Recherche en Biologie Forestiere
             Universite Laval
             Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
             Fax: 418 656 7493
             Email: jmackay@rsvs.ulaval.ca
             Center for Computational Genomics and Bioinformatics (CCGB),
             University of Minnesota, MN id Identifier: MN517370I Clone ID:
             GQ0083_H02 Clones available through: John MacKay, Ph. D. Professeur
             adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
             de Recherche en Biologie Forestiere (Forest Biology Research
             Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
             Plate: 3 row: 02 column: H
             Seq primer: M13 Reverse Primer.
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                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide

VERSION     CO472761.1  GI:50141306
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1 (bases 1 to 803)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN id Identifier: MN198052 Clone ID:
            GQ0081.BR_G07 Clones available through: John MacKay, Ph. D.
            Professeur adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca
            Centre de Recherche en Biologie Forestiere
            (Forest Biology Research Center) Universite Laval Quebec, Quebec
            CANADA G1K 7P4
            Plate: 1.BR  row: 07  column: G
            Seq primer: M13 Reverse Primer.
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                     /sex="Hermaphrodite"
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                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"
                     /dev_stage="Vascular cambium, secondary phloem, and bark
                     from trees harvested 1 and 7 days after girdling
                     treatment"
                     /lab_host="E. coli DH10B cells"
                     /clone_lib="GQ008: Cambium, phloem and bark of girdled
                     saplings"
                     /note="Organ: Main stem of 4 year old saplings,
                     approximately 60 cm tall; Vector: pBluescript II SK (+)
                     XR; Site 1: Eco-RI; Site 2: Xho-I; Tissues were pooled
                     from above and below the girdle. cDNA was prepared from 5
                     mg of poly A+ selected RNA and was directionally ligated
                     into the pBluescript II SK (+) XR vector (Stratagene),
                     transformed by electroporation into DH10B cells (in
                     vitrogen) for propagation"
ORIGIN

Query Match      74.3%;  Score 546.6;  DB 8;  Length 803;
Best Local Similarity   94.7%;   Pred. No. 2.8e-160;
Matches  577;  Conservative   0;  Mismatches  29;  Indels   3;  Gaps   1;

Qy  121 AGTAGAGACTTTCAACAAGGGTAATATCGGGAAACCTCCTCGGATCCATTGCCCAGCT 180
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Db   31 ATTGAGACTTTTCAACAAGGGTAATAATCCGGAACCTCCTCGGATTCCATTGCCCAGCT 90

Qy  181 ATCTGTCACTTCATCAAAAGGACGTAGAAAAAGGACACGTAGGTGGCACCTACAAAATGCCATCAT 240
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Db   91 ATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCCTCCTACAAAATGCCATCAT 150

Qy  241 TGCCATAAAGGAGAAGAAAAGGCTATCCGTTCAAAGATGCCTCTGCCGGACACGTAGGTCCCAAAGATGGA 300
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Db  151 TGCCGATAAAGGAGAAAGGGCCCATCGTTGCAGATGCCTCTGCCCGCAGTGGGTCCCAAAGATGGA 210

Qy  301 CCCCCACCCAGGAGGAGCCATCGTGTGGAAAAAAGAAGAGGAGCAGTCGCGTTCCAAAGCAA 360
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Db  211 CCCCCACCCAGGAGGAGCCATCGTGTGGAAAAAAGAGAGAGCAGTTCCAACCCACGGTCTTCAAAGGCAA 270

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RESULT 5
CK437984
LOCUS       CK437984    713 bp    mRNA    linear    EST 08-JAN-2004
DEFINITION  GQ0081.BR_K09 GQ008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GQ0081_K09 5', mRNA sequence.
ACCESSION   CK437984
VERSION     CK437984.1  GI:40768543
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1 (bases 1 to 713)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN id Identifier: MN1718650 Clone ID:
            GQ0081.K09 Clones available through: John MacKay, Ph. D. Professeur
            adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
            de Recherche en Biologie Forestiere (Forest Biology Research
            Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
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            Seq primer: M13 Reverse Primer.
FEATURES             Location/Qualifiers
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                     /clones="GQ0081_K09"
                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"

Qy  361 GTGGATTGAGTGAATTG---CAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTC 417
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Qy  418 CTCGGATTCCATTGCCCAGCTACTCTTCATCTCAACTTCATCAAAAGGACAGTAGAAAAAGGACACGT 477
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Qy  478 GGCACCTACAAAATGCCATCATTCGGATAAAAAGGAGCTATCGTTCAAGATGCCTCTGCCC 537
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Db  391 GGCTCCTACAAAATGCCATCATTCGGATAAAAGGGCCATCGTTGCAAGATGCCTCTGCC 450

Qy  538 GACACGTAGGTCCCAAAGATAGGACCCCCCACCCACGGAGGAGCGATCGTGCGGAAAAAAGAAGACGTT 597
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Db  451 GACACGTGGTCCCAAAGATGGACCCCCACCCACGGAGGAGCATCGTGGAAAAAAGAAGAGCGTT 510

Qy  598 CCAACCACGTCTTCAAACGAACAAGTGGATTGATCTGATATTCCACTGACGTAAGGAGAGAT 657
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Db  571 GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGAAGTTCATTTCATTTG 630

Qy  718 GAGAGGACA 726
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Db  631 GAGAGGAGA 639

KEYWORDS   EST.
SOURCE     Picea glauca (white spruce)
ORGANISM   Picea glauca
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE  1 (bases 1 to 741)
AUTHORS    Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
           Retzel,B., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
           Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
TITLE      Arborea EST sequencing in Picea glauca (white spruce)
JOURNAL    Unpublished (2004)
COMMENT    Contact: John MacKay
           Centre de Recherche en Biologie Forestiere
           Universite Laval
           Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
           Fax: 418 656 7493
           Email: jmackay@rsvs.ulaval.ca
           Center for Computational Genomics and Bioinformatics (CCGB),
           University of Minnesota, MN Id Identifier: MN5173771 Clone ID:
           GQ0083.J24 Clones available through: John MacKay, Ph. D. Professeur
           adjoinE -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
           de Recherche en Biologie Forestiere (Forest Biology Research
           Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
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           Seq primer: M13 Reverse Primer.
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                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"
                     /dev_stage="Vascular cambium, secondary phloem, and bark
                     from trees harvested 1 and 7 days after girdling
                     treatment"
                     /lab_host="E. coli DH10B cells"
                     /clone_lib="GQ008: Cambium, phloem and bark of girdled
                     saplings"
                     /note="Organ: Main stem of 4 year old saplings.
                     approximately 60 cm tall; Vector: pBluescript II SK (+)
                     XR; Site_1: Eco-RI; Site_2: Xho-I; tissues were pooled
                     from above and below the girdle. cDNA was prepared from 5
                     mg of poly A+ selected RNA and was directionally ligated
                     into the pBluescript II SK (+) XR vector (Stratagene),
                     transformed by electroporation into DH10B cells (in
                     vitrogen) for propagation"
ORIGIN

Query Match    74.0%;  Score 544.6;  DB 5;  Length 741;
Best Local Similarity  94.4%;  Pred. No. 1.2e-159;
Matches 575;  Conservative   0;  Mismatches  31;  Indels    3;  Gaps    1;

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Qy     241 TGGGATAAAGGAAAGGCTATCGTTCAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGA 300
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RESULT 7
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DEFINITION  GQ0081.BR_F05 GQ0008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GQ0081_F05 5', mRNA sequence.
ACCESSION   CK437920
VERSION     CK437920.1  GI:40768406
KEYWORDS    EST.
SOURCE      Picea glauca
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1  (bases 1 to 655)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN id identifier: MNS171736 Clone ID:
            GQ0081_F05 Clones available through: John MacKay, Ph. D. Professeur
            adjoint - Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
            de Recherche en Biologie Forestiere (Forest Biology Research
            Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
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                     of trees girdled by removing a ring of bark ca. 1 cm wide
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                     from trees harvested 1 and 7 days after girdling
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Query Match        73.0%;  Score 537.2; DB 5;  Length 655;
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Matches  567;  Conservative  0;  Mismatches  43;  Indels  3;  Gaps  1;
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Qy   337 CTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGT 396
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Db   337 CTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTAGAAAAAGGAAGGT 396

Qy   397 GGCTCCTACAAATGCCATCATTGCGATTAAAGGAAAGGCCATCGTTCAAGAATGCCTCTGC 456
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   397 GGCTCCTACAAATGCCATCATTGCGATTAAAGGAAAGGCCATCGTTCAAGAATGCCTCTGC 456

Qy   457 GACAGTGGTCCCAAAGATGGACCCCCACCCAGCGAGCGATCGTTGGAAAAAGAAGACGTT 516
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   457 GACAGTGGTCCCAAAGATGGACCCCCACCCAGCGAGCGATCGTTGGAAAAAGAAGACGTT 516

Qy   517 CCAACCACGGTCTTCAAAGCAAGTGGATTGATTGATATCTCCACTGAGGTAAGGGATGAC 576
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   517 CCAACCACGGTCTTCAAAGCAAGTGGATTGATTGATATCTCCACTGAGGTAAGGGATGAC 576

Qy   577 GCACAATCCCACTATCCTTCCGCAAGACCCTTCCCTATATAAGGAAGTTCATTTCATTG 636
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   577 GCACAATCCCACTATCCTTCCGCAAGACCCTTCCCTATATAAGGAAGTTCATTTCATTG 636

Qy   637 GAGAGGAGA 645
         |||||||
Db   637 GAGAGGAGA 645

RESULT 8
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LOCUS       CK438485                  736 bp    mRNA     linear      EST 29-JUN-2005
DEFINITION  GQ0085.BR_M24 GQ0008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GenomeQuebec_Id:GQ0085M24 5', mRNA
            sequence.
ACCESSION   CK438485
VERSION     CK438485.1  GI:40769782
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
```

Qy   144 TGGGATAAAGGAAAGGCCATTCGTTCAAGATGGCCTCTGCCCGGACAGTGGTCCCAAGATGGA 203
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   144 TGGGATAAAGGAAAGGCCATTCGTTCAAGATGGCCTCTGCCCGGACAGTGGTCCCAAGATGGA 203

Qy   204 CCCCCACCCAGCAGGAGCATCGTCCTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAGCA 263
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   204 CCCCCACCCAGCAGGAGCATCGTCCTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAGCA 263

Qy   264 GTGGATTGATGTGATG---CAGTGAGACTTTTCAACAAAGGGTAATATCCGGAAAAACCTC 323
         |||||||||||||||   |||||||||||||||||||||||||||||||||||||||||||
Db   264 GTGGATTGATGTGATGTTCCAGTGAGACTTTTCAACAAAGGGTAATATCCGGAAAAACCTC 323

Qy   324 CTCGGATTCCATTGCCCAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAAAGGAAGGT 383
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   324 CTCGGATTCCATTGCCCAGCTATCTGTCACTTATTTGTGAAGATAGTGGAAAAAGGAAGGT 383

Qy   384 GGCTCCTACAAATGCCATCATTGCGATTAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC 443
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   384 GGCTCCTACAAATGCCATCATTGCGATTAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCC 443

Qy   444 GACAGTGGTCCCAAAGATGGACCCCCACCCAGCGAGCGATCGTTGGAAAAAGAAGACGTT 503
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   444 GACAGTGGTCCCAAAGATGGACCCCCACCCAGCGAGCGATCGTTGGAAAAAGAAGACGTT 503

Qy   504 CCAACCACGTCTTCAAAGCAAGTGGATTGATTGATATCTCCACTGAGGTAAGGGATGAC 563
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   504 CCAACCACGTCTTCAAAGCAAGTGGATTGATTGATATCTCCACTGAGGTAAGGGATGAC 563

Qy   564 GCACAATCCCACTATCCTTCCGCAGACCCTTCCCTATATAAGGAAGTTCATTTCATTTG 623
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   564 GCACAATCCCACTATCCTTCCGCAGACCCTTCCCTATATAAGGAAGTTCATTTCATTTG 623

Qy   624 GAGANNNNNNNNT 636
         ||||
Db   624 GAGAGGACACGCT 730

Qy   718 GAGAGGACACGCT 730
         |||||||
Db   637 GAGAGGAGA 645

```
Qy  418  CTCGGATTCCATTGCCCAGCTATCGTCACTCATCAAAACGACAGTAGAAAAGGAAGGT  477
         |||||||||||||||||||||||||||||| || ||||  ||||||||||||||||||
Db  340  CTCGGATTCCATTGCCCAGCTATCGTCACTTATTGTGAAGATAGTGGAAAAGGAAGGT  399

Qy  478  GGCACCTACAAAATGCCATCATTGGCGATAAAGGGCTATCGTTCAAGATGCCCTGCC  537
         |||  |||||| |||||||||||||||||||||||  ||||||||| |||||||||||
Db  400  GGGTCCTACAAATGCCATCATTGGCGATAAAGGAAAGGCCATCGTTGAAGATGCCCTGCC  459

Qy  538  GACAGTGGTCCAAAGATGACCCCACCACGAGGAGCATCGTGGAAAAAGAAGACGTT  597
         |||||||||||  |||||||||||| |||||||||||||||||||||||||||||||
Db  460  GACAGTGGTCCCAAAGATGACCCCCACCCCACGAGGAGCATCGTGGAAAAAGAAGACGTT  519

Qy  598  CCAACCGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGAC  657
         ||||||  |||||||||||||||||||||||||||||||||||| |||||||||||||
Db  520  CCAACCACGTTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACGACGTAAGGGATGAC  579

Qy  658  GCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCA  713
         ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db  580  GCACAATCCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCA  635
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RESULT 9
CK438348
LOCUS       CK438348     698 bp    mRNA    linear   EST 29-JUN-2005
DEFINITION  GQ0085.BR_D16 GQ008: Cambium, phloem and bark of girdled saplings
            Picea glauca cDNA clone GenomeQuebec_Id:GQ008SD16 5', mRNA
            sequence.
ACCESSION   CK438348
VERSION     CK438348.1   GI:4076 9405
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R. Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN_id identifier: MN5174387 Clone ID:
            GQ0085_D16 Clones available through: John MacKay, Ph. D. Professeur
            adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
            de Recherche en Biologie Forestiere (Forest Biology Research
            Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
            Plate: 5  row:16  column: D
            Seq primer: M13 Reverse Primer.
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                     /mol_type="mRNA"
                     /strain="pg-653"
                     /db_xref="taxon:3330"
                     /clone="GenomeQuebec_Id:GQ008SD16"
                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"
                     /dev_stage="Vascular cambium, secondary phloem, and bark
                     from trees harvested 1 and 7 days after girdling
                     treatment"
                     /lab_host="E. coli DH10B cells"
                     /clone_lib="GQ008: Cambium, phloem and bark of girdled
                     saplings"
                     /note="Organ: Main stem of 4 year old saplings,

ORGANISM    Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1  (bases 1 to 736)
  AUTHORS   Morency,M.-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
COMMENT     Contact: John MacKay
            Centre de Recherche en Biologie Forestiere
            Universite Laval
            Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
            Fax: 418 656 7493
            Email: jmackay@rsvs.ulaval.ca
            Center for Computational Genomics and Bioinformatics (CCGB),
            University of Minnesota, MN_id identifier: MN5174611 Clone ID:
            GQ0085_M24 Clones available through: John MacKay, Ph. D. Professeur
            adjoint -Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
            de Recherche en Biologie Forestiere (Forest Biology Research
            Center) Universite Laval Quebec, Quebec CANADA G1K 7P4
            Plate: 5  row: 24  column: M
            Seq primer: M13 Reverse Primer.
FEATURES             Location/Qualifiers
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                     /organism="Picea glauca"
                     /mol_type="mRNA"
                     /strain="pg-653"
                     /db_xref="taxon:3330"
                     /clone="GenomeQuebec_Id:GQ0085M24"
                     /sex="Hermaphrodite"
                     /tissue_type="Vascular cambium, secondary phloem and bark
                     of trees girdled by removing a ring of bark ca. 1 cm wide
                     from the midpoint of the main stem"
                     /dev_stage="Vascular cambium, secondary phloem, and bark
                     from trees harvested 1 and 7 days after girdling
                     treatment"
                     /lab_host="E. coli DH10B cells"
                     /clone_lib="GQ008: Cambium, phloem and bark of girdled
                     saplings"
                     /note="Organ: Main stem of 4 year old saplings,
                     approximately 60 cm tall; Vector: pBluescript II SK (+)
                     XR, Site_1: Eco-RI; Site_2: Xho-I; Tissues were pooled
                     from above and below the girdle. cDNA was prepared from 5
                     mg of poly A+ selected RNA and was directionally ligated
                     into the pBluescript II SK (+) XR vector (Stratagene),
                     transformed by electroporation into DH10B cells (in
                     vitrogen) for propagation"

ORIGIN
Query Match     72.7%;  Score 535.2;  DB 5;  Length 736;
Best Local Similarity   94.8%;  Pred. No. 1e-156;
Matches  565;  Conservative    0;  Mismatches  28;  Indels   3;  Gaps   1;

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Qy  121  AGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTTCGGATTCCATTGCCCAGCT  180
         |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db   40  ATTGAGACTTTCAACAAAGGGTAATATCCGGAAACCTCCTTCGGATTCCATTGCCCAGCT   99

Qy  181  ATCTGTCACTTCATCAAAACGACAGTAGAAAAGGAAGGTGCACCTACAAAATGCCATCAT  240
         ||||||||||| || |  |  ||||| |||||||||||||||  ||||||||||||||||
Db  100  ATCTGTCACTTATTGTGAAGATAGTGGAAAAGGAAGGTGCCTCCTACAAAATGCCATCAT  159

Qy  241  TGGCGATAAAGGGCTATCGTTCAAGATGCCCTGCCGACAGTGGTCCAAAGATGGA  300
         ||||||||||||  | ||||||| |||||||||||||||||||||||  |||||||
Db  160  TGGCGATAAAGGAAAGGCCATCGTTGAAGATGCCCTGCCGACAGTGGTCCCAAAGATGGA  219

Qy  301  CCCCACCACGAGGAGCATCGTGGAAAAAGGAAGACGTTCCAACCACGTCTTCAAAGCAA  360
         |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  220  CCCCACCCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA  279

Qy  361  GTGGATTGATGTGATTG---CAGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTC  417
         |||||||||||||||| |     |||||||||||||||||||||||||||| |||||||||
Db  280  GTGGATTGATGTGATGTGATGTCCCATTGACTTTTCAACAAAGGGTAATATCCGGAAACCTC  339
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## Left block (RESULT 10)

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RESULT 10
LOCUS       CO481168               610 bp    mRNA     linear   EST 29-JUN-2005
DEFINITION  GQ0165.B7_M24 GQ016: Primary, secondary SHOOT -N fertil. Treatments
            Picea glauca cDNA clone GenomeQuebec_Id:GQ0165M24 3', mRNA
            sequence.
ACCESSION   CO481168
VERSION     CO481168.1  GI:50160512
KEYWORDS    EST.
SOURCE      Picea glauca (white spruce)
  ORGANISM  Picea glauca
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Morency,M-J., Cooke,J., Pavy,N., Parsons,L., Paule,C., Seguin,A.,
            Retzel,E., Butterfield,Y., Barber,S., Yang,G., Stott,J.,
            Siddiqui,A., Holt,R., Marra,M. and MacKay,J.
  TITLE     Arborea EST sequencing in Picea glauca (white spruce)
  JOURNAL   Unpublished (2004)
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ORIGIN

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Query Match      72.4%;  Score 533.2;  DB 5;  Length 698;
Best Local Similarity   94.5%;  Pred. No. 4.4e-155;
Matches 563;  Conservative    0;  Mismatches 30;  Indels    3;  Gaps    1;

Qy        121 AGTGAGCACTTTCAACAAAAGGTAATACCGGAAACCCTCCCGGATTCCATTGCCCAGCT 180
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Db         37 ATTGAGACTTTTCAACAAGGGTAATATCCGGAAACCCTCCCGGATTCCATTGCCCAGCT 96

Qy        181 ATCTGTCACTTCATCAAAAGGACAGTAGAAAAACGAAGGTGGCACCTTACAAAATGCCATCAT 240
Db         97 ATCTGTCACTTTATTGTAGAGATAGTGTGAAAAAGGAAGGTGGCCTCCTACAAAATGCCATCAT 156

Qy        241 TGCGATAAAGAGAAAGGCTATCGTTCAAGATGACTGCTTGCCCGACAGTGGTCCCAAAGATGGA 300
Db        157 TGCGATAAAGAGAAAGGCCATCGTTGAAGATGCCTTGCCCGACAGTGGTCCCAAAGATGGA 216

Qy        301 CCCCCACCCAGCGAGGAGCATGCTGGTGAAAAAGAAGACGTTCCACCACGTCTTCAAAGCAA 360
Db        217 CCCCCACCCCAGCGAGGAGCATCCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCA 276

Qy        361 GTGGATTCGANTCGTGATTG---CAGTGAGACTTTTCAACAAGGGTAATATCCGGAAACCTTC 417
Db        277 GTGGATTCGATGATCGGTCCGATTCAGACACTTTTCAACAAGGGTAATATCCGGAAACCTC 336

Qy        418 CTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTCAAAAGGACACTAGAAAAAGGAAGGT 477
Db        337 CTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATACGTGAAAAAGGAAGGT 396

Qy        478 GGCACCTACAAAATGCCATCATTGCGATAAAAGAGAAAGGCTATCGTTCAAGATGCCTTGCC 537
Db        397 GGCTCCTACAAAATGCCATCATTGCGATAAAGAGAAAGGCCATCGTTGAAGATGCCTTGCC 456

Qy        538 GACAGTGGTCCCAAAGATGGACCCCCACCCACCGAGGAGCATCGTGGAAAAAGAAGACGTT 597
Db        457 GACAGTGGTCCCAAAGATGGACCCCCACCCAGCGAGGAGCATCGTGGAAAAAGAAGACGTT 516

Qy        598 CCAACCACGTCTTCAAAGCAACGTGGATTGATTGATTGATCTCCCACTGAGCTGACGTAAGGCGATGAC 657
Db        517 CCAACCACGTCTTCAAAGCAACGTGGATTGATTGATCTCCCACTGAGCTGACGTAAGGCGATGAC 576

Qy        658 GCACAATCCCACTATCCTCGCGAGGACCCTTTCCTCTATATAAGGAAGGTTCATTTCA 713
Db        577 GCACAATCCCACTATCCTTCGCGAGAGANNCTTCCTCTATATAAGGAAGGTTCATTTCA 632
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## Right block (RESULT continued)

COMMENT
```
Contact: John MacKay
Centre de Recherche en Biologie Forestiere
Universite Laval
Pavillon Charles-Eugene Marchand, Quebec, Quebec, CANADA G1K 7P4
Fax: 418 656 7493
Email: jmackay@rsvs.ulaval.ca
Center for Computational Genomics and Bioinformatics (CCGB),
University of Minnesota, MN Id Identifier: MN5268594  Clone ID:
GQ0165_M24 Clones available through: John MacKay Ph. D. Professeur
adjoint-Assistant professor EMAIL: jmackay@rsvs.ulaval.ca Centre
de Recherche en Biologie Forestiere [Forest Biology Research
Center] Universite Laval Quebec, Quebec CANADA G1K 7P4
Seq primer: T7 Primer;
Plate: 5  row: 24  column: M
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FEATURES             Location/Qualifiers
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                /db_xref="taxon:3330"
                /clone="GenomeQuebec_Id:GQ0165M24"
                /sex="Hermaphrodite"
                /tissue_type="Xylem, pith, cambium, phloem, bark"
                /dev_stage="Primary & secondary shoot, secondary phloem
                pooled from plants fertilized with low and high NH4NO3"
                /lab_host="E. coli DH10B cells"
                /clone_lib="GQ016: Primary, secondary SHOOT -N fertil.
                Treatments"
                /note="Organ: Main stem region producing secondary growth
                on 60 cm tall seedlings; Vector: pBluescript II SK (+) XR;
                Site 1: Eco-RI; Site 2: Xho-I; cDNA was prepared from 5 mg
                of poly A+ selected RNA and was directionally ligated into
                the pBluescript II SK (+) XR vector (Stratagene),
                transformed by electroporation into DH10B cells (In
                vitrogen) for propagation"
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ORIGIN
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Query Match      65.3%;  Score 480.8;  DB 8;  Length 610;
Best Local Similarity   93.6%;  Pred. No. 1.3e-139;
Matches 510;  Conservative    0;  Mismatches 32;  Indels    3;  Gaps    1;

Qy        185 GTCACTTCATCAAAAGGACACAGTAGAAAAACGAAGGTGGCACCTACAAAATGCCATCATTCG 244
                | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCACTTTATTGTGAAGATAGTGTGAAAAAGGNNNNNGGCTCCTACAAAATGCCATCATTCG 60

Qy        245 ATAAAGAGAAAGGCTATCGTTCAAGATGCCTTGCGGCGACAGTGGTCCCAAAGATGGACCCC 304
Db         61 ATAAAGAGAAAGGCCATCGTTGAAGATGCCTTGCCCGACAGTGGTCCCAAAGATGGACCCC 120

Qy        305 CACCCACCGAGGAGCATCGTGGAAAAAGAAGACGTTCCACCACGTCTTCAAAGCAAGTGG 364
Db        121 CACCCACCCAGCGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGG 180

Qy        365 ATTGATTGATTGATCTCCAACTGAGCTGACGTAATATCCGGAACCCCTCCCCG 421
Db        181 ATTGATTGATGTCCGATTCAGACACTTTTCAACAAGGGTAATATCCGGAAACCCTCCTCG 240

Qy        422 GATTCCATTGCCCAGCTATCTGTCACTTTATTGTCAAGACACGTAGAAAAGCAGTAGGCCA 481
Db        241 GATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGAAAAAGGAAGGTGGCA 300

Qy        482 CCTACAAAATGCCATCATTGCGATAAAAGAGAAAGGCTATCGTTCAAGATGCCTTCGCCGACA 541
Db        301 CCTACAAAATGCCATCATTGCGATAAAGAGAAAGGCCATCGTTGAAGATGCCTTGCCCGACA 360

Qy        542 GTGGTCCCAAAGATGGACCCCCACCCACCGAGGAGCATCGTGGAAAAAGAAGACGTTCCAA 601
Db        361 GTGGTCCCAAAGATGGACCCCCACCCAGCGAGGAGCATCGTGGAAAAAGAAGACGTTCCAA 420

Qy        602 CCACGTCTTCAAAGCAAGTGGAATTGGAATTGAATTGGATTGATTGATCTCCACTGAGCTGACGTGACGCAC 661
Db        421 CCACGTCTTCAAAGCAAGTGGAATTGGAATTGATTAATCTCCACTGAGCTGACGTAAGGGATGACGCAC 480
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Qy  241 TCGGATAAAGGAAAGGCTATCGTTCAGATGGCTTCGCCGACAGTCGTCCAAAGATGGA 300
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Db  214 TCGGATAAAGGAAAGGCCATCGTTGAGATGGCATGGCCGGCGACAGTGCTCCAAAGATGGA 273

Qy  301 CCCCACCCACGAGGAGCATCGTCGGAAAAAGACGTTCAACCAGTCTTCAAAGCAA 360
         |||||||||||||||||||||||| ||||||||||||||||||||||||||
Db  274 CCCCACCCACGAGGAGCATCGTGGAAAAAGAGACGTTCAACCACGTCTTCAAAGCAA 333

Qy  361 GTGGATTGATGTGATTGC------------------------ 378
         |||||| | |
Db  334 GTCGATTGATGTGATAACATGGTGAGCACGACACACTTGTCTACTCCAAAATATCAAA 393

Qy  379 ------------AGTGAGACTTTTCAACAAAGGGTAATATCGGGA 411
                     | ||||||||||||||||||||||
Db  394 GATACAGTCTCAGAAGACCAAAGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGA 453

Qy  412 AACCTCCTCGGATTCCATTGCCAGCTATCGTCACTTCATCAAAAGACAGTAGAAAAG 471
         |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  454 AACCTCCTCGGATTCCATTGCCCAGCTATCGTCACTTTATTGTGAAGATAGTGGAAAAG 513

Qy  472 GAAGGTGGCACCTACAAATGCCATCATTGCGATAAAGGAAAGGCTATCGTTCAAGATGCC 531
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Db  514 GAAGGTGGCTCCTACAAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCC 573

Qy  532 TCTGCGCACAGTGGTCCCAAAGATGGACCCCCACCACGAGGAGCATCCTGGAAAAAAGAA 591
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Db  574 TCTGCGCAGGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCACGTGGAAAAAAAGAA 633

Qy  592 GACGTTCCAACCAGTCTTCAAAGCAAGCAAGTGGATTGATGTGATATCCTCACTGACGTAAGG 651
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Db  634 GACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGG 693

Qy  652 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCT 691
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Db  694 GATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCT 733

RESULT 12
DN381521/c
LOCUS       DN381521                 738 bp    mRNA    linear    EST 07-MAR-2005
DEFINITION  LIB38534_042_E11_T7_1 LIB38534 Canis familiaris cDNA clone
            LIB38534_42_E11, mRNA sequence.
ACCESSION   DN381521
VERSION     DN381521.1  GI:60562741
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1 (bases 1 to 738)
  AUTHORS   Staten,N.R.
  TITLE     Direct Submission (Staten,N.R.)
  JOURNAL   Unpublished (2005)
  COMMENT   Contact: Nick Staten
            Tel: 636 247 6855
            Email: nicholas.r.staten@pfizer.com.
FEATURES             Location/Qualifiers
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                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="LIB38534_42_E11"
                     /tissue_type="unknown"
                     /lab_host="DH10B"
                     /clone_lib="LIB38534"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI"
ORIGIN

Query Match             55.0%;  Score 405;  DB 9;  Length 738;
Best Local Similarity   96.0%;  Pred. No. 1e-115;
Matches  427; Conservative   0; Mismatches  15; Indels  3; Gaps  1;

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Qy  662 AATCCCACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGA 721
         ||||||||||||||||||||||||||||||||||||||||||||
Db  481 AATCCCACTATCCTTCGCAAGACCCCTCCTCTATATAAGGAAGTTCATTTCATTTGGAGA 540

Qy  722 GGACA 726
         ||| |
Db  541 GGAGA 545

RESULT 11
CX308688
LOCUS       CX308688                 733 bp    mRNA    linear    EST 06-MAY-2005
DEFINITION  C21002G02Rv AbsLeaSub1 Citrus clementina cDNA clone C21002G02, mRNA
            sequence.
ACCESSION   CX308688
VERSION     CX308688.1  GI:63077542
KEYWORDS    EST.
SOURCE      Citrus clementina
  ORGANISM  Citrus clementina
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Sapindales; Rutaceae; Citrus.
REFERENCE   1 (bases 1 to 733)
  AUTHORS   Forment,J., Gadea,J., Huerta,L., Abizanda,L., Agusti,J., Alamar,S.,
            Alos,E., Andres,F., Arribas,R., Beltran,J.P., Berbel,A.,
            Blazquez,M.A., Brumos,J., Canas,L.A., Cercos,M.,
            Colmenero-Flores,J.M., Conesa,A., Estables,B., Gandia,M.,
            Garcia-Martinez,J.L., Gimeno,J., Gisbert,A., Gomez,G.,
            Gonzalez-Candelas,L., Granell,A., Guerri,J., Lafuente,M.T.,
            Madueno,F., Marcos,J.F., Marques,M.C., Martinez,F.,
            Martinez-Godoy,M.A., Miralles,S., Moreno,P., Navarro,L., Pallas,V.,
            Perez-Amador,M.A., Perez-Valle,J., Pons,C., Rodrigo,I.,
            Rodriguez,P.L., Royo,C., Serrano,R., Soler,G., Tadeo,F., Talon,M.,
            Tezol,J., Trenor,M., Vaello,L., Vicente,O., Vidal,Ch., Zacarias,L.
            and Conejero,V.
  TITLE     Development of a citrus genome-wide EST collection and cDNA
            microarray as resources for genomic studies
  JOURNAL   Plant Mol. Biol. 57 (3), 375-391 (2005)
  PUBMED    15830128
  COMMENT   Contact: Forment J
            Genomics Laboratory
            Instituto de Biologia Molecular y Celular de Plantas (Universidad
            Politecnica de Valencia - Consejo Superior de Investigaciones
            Cientifica)
            Avenida de los Naranjos s/n, 46022 Valencia, Spain
            Email: jforment@ibmcp.upv.es.
FEATURES             Location/Qualifiers
     source          1..733
                     /organism="Citrus clementina"
                     /mol_type="mRNA"
                     /cultivar="Clemenules"
                     /db_xref="taxon:85681"
                     /clone="C21002G02"
                     /sex="thermaphrodite"
                     /dev_stage="adult trees"
                     /lab_host="Escherichia coli"
                     /clone_lib="AbsLeaSub1"
                     /note="Organ: leaves; Vector: pCR2.1; Subtracted cDNA
                     library made from laminar abscision zone of leaves"
ORIGIN

Query Match             60.8%;  Score 447.2;  DB 8;  Length 733;
Best Local Similarity   84.8%;  Pred. No. 5.3e-129;
Matches  543; Conservative   0; Mismatches  28; Indels  69; Gaps  1;

Qy  121 AGTGGAGACTTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 180
         || |||||||||||||||||||||||||| |||||||||||||||||||||||||
Db   94 ATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGAAACCTCCTCGGATTCCATTGCCCAGCT 153

Qy  181 ATCGTCACTTCATCAAAAGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 240
         ||||||||| || |||| |||||| | ||||||||| || | ||||||||||||||
Db  154 ATCGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAAATGCCATCAT 213

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Qy    290  CCAAAGATGGACCCCCACGAGGAGCATCGTGGAAAAAGAAGAAGCGTTCCAACCACGT 349
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    738  CCAAAGATGGACCCCCACGAGGAGCATCGTGGAAAAAGAAGAAGCGTTCCAACCACGT 679

Qy    350  CTTCAAAGCAAGTGAGATTGAATTGATATG----CAGTAGGACTTTTCAACAAAGGTAAAT 406
           |||||||||||||||||||||||||||||    |||||||||||||||||||||||
Db    678  CTTCAAAGCAAGTGAGATTGAATTGATATGTCCGGATTGAGAGACTTTTCAACAAAGGTAATAT 619

Qy    407  CGGGAAACCTCCCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTTG 466
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    618  CCGGAAACCTCCCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAAGGACAGTTG 559

Qy    467  AAAAAGGAAGGTGGCACCTACAAATGCCATCATCCATTGCCATAAGAAGGAAAGGCTTATCGTTCAAG 526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    558  AAAAGGAAGGTGGCCTCCTACAAATGCCATCATTGGCATAAGAAGGAAAGGCCATCGTTCAAG 499

Qy    527  ATGCTCTGCCGACAGTGGTTCCCAAAGATGGACCCCCACCCAGACGAGGAGGACATCGGTCGGTGGAA 586
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    498  ATGCCTCTGCCGACAGTGTCCCAAAGATGGACCCCCACCCAGACGAGGAGGACATCGGTCGGTGGAA 439

Qy    587  AAGGAGAGAGTTCCAACCACGTTCAAAGCAAGTGAGATTGATGATAATCTTCCACTGACG 646
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    438  AAGGAGAGAGCGTTCCAACCACGTTCAAAAGCAAGTGAGATTGATGATAATCTTCCACTGACG 379

Qy    647  TAAGGGATGAGCAGCACAATCCCACTATCCTTCCTCCTTCTTATATAATAAGGAAGTTT 706
           |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    378  TAAGGGATGAGCAGCACAATCCCACTATCCTTCCTCCTTCTTATATAATAAGGAAGTTT 319

Qy    707  CATTTCATTTGGAGAGGACAGGCTG 731
           |||||||||||||||||||||||||
Db    318  CATTTCATTTGGAGAGGACAGGCTG 294
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RESULT 13

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DN381910/c
LOCUS           DN381910                     685 bp    mRNA      linear    EST 07-MAR-2005
DEFINITION      LIB38534_041_C01_T7_1 LIB38534 Canis familiaris cDNA clone
                LIB38534_41_C01, mRNA sequence.
ACCESSION       DN381910
VERSION         DN381910.1  GI:60563130
KEYWORDS        EST.
SOURCE          Canis familiaris (dog)
ORGANISM        Canis familiaris
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                Canis.
REFERENCE       1  (bases 1 to 685)
AUTHORS         Staten,N.R.
TITLE           Direct Submission (Staten,N.R.)
JOURNAL         Unpublished (2005)
COMMENT         Contact: Nick Staten
                Tel: 636 247 6855
                Email: nicholas.r.staten@pfizer.com.
FEATURES             Location/Qualifiers
     source          1..685
                     /organism="Canis familiaris"
                     /mol_type="mRNA"
                     /db_xref="taxon:9615"
                     /clone="LIB38534_41_C01"
                     /tissue_type="unknown"
                     /lab_host="DH10B"
                     /clone_lib="LIB38534"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI"
ORIGIN
Query Match        48.1%;  Score 354;  DB 9;  Length 685;
Best Local Similarity  95.4%;  Pred. No. 1.1e-99;
Matches  376;  Conservative  0;  Mismatches  15;  Indels  3;  Gaps  1;

Qy    341  CAACCACGTTCTCAAAGCAAGTGAGATTGAATTGATATGATGTGC---AGTAGGACTTTTCAACAA 397
           ||||||||||||||||||||||||||||||||||||||||||||   |||||||||||||||
Db    685  CAACCACGTTCTCAAAGCAAGTGAGATTGAATTGATATGGTCGCCGATTGAGACTTTTCAACAA 626
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```
Qy    398  GGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTCATCAAAA 457
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    625  GGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGA 566

Qy    458  GGACAGTTAGGAAAGGAGAGGGTGGGCACCTACAAATGCCATCATTGCCATAAGAAGAAAGGCTA 517
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    565  AGATAGTGTAGGAAAGGAGAGGTGGCTCCCTACAAATGCCATCATTGGCATAAGAAGGAAAGGCCA 506

Qy    518  TCGGTCAAGATGCTCTGCCGACAGTGGTTCCCAAAGATGGACCCCCACCCAGACGAGGAGGACA 577
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    505  TCGTTGAAGATGCTCTGCCGACAGTGTCCCAAAGATGGACCCCCACCCAGACGAGGAGGACA 446

Qy    578  TCGGTCGGAAAAAGGAGAGAGCGTTCCAACCACGTTCAAAGCAAGTGAGATTGATGTGATATCT 637
           ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    445  TCGGTCGGAAAAAGGAGAGAGCGTTCCAACCACGTTCAAAGCAAGTGAGATTGATGTGATATCT 386

Qy    638  CCACTGACGTAGGGGATGAGCCACAATCCCACTATCCTTCCTCCGAAGACGCCTTTTCCTCTATAT 697
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    385  CCACTGACGTAGGGGATGAGCGACAATCCCACTATCCTTCGAAGACGCCTTTTCCTCTATAT 326

Qy    698  AAGGAAGTTCATTTCATTTGGAGAGGACAGGCTG 731
           ||||||||||||||||||||||||||||||||||
Db    325  AAGGAAGTTCATTTCATTTGGAGAGGACAGGCTG 292
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RESULT 14

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AQ362115
LOCUS           AQ362115                     839 bp    DNA       linear    GSS 03-FEB-1999
DEFINITION      mgxb0003F18f CUGI Rice Blast BAC library Magnaporthe grisea genomic
                clone mgxb0003F18f, genomic survey sequence.
ACCESSION       AQ362115
VERSION         AQ362115.1  GI:4211034
KEYWORDS        GSS.
SOURCE          Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM        Magnaporthe grisea
                Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina; Sordariomycetes;
                Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
REFERENCE       1  (bases 1 to 839)
AUTHORS         Yu,Y., Zhu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
                Phillips,K., Sasinowski,M, Wing,R.A. and Dean,R.A.
TITLE           A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                Genome
JOURNAL         Unpublished (1998)
COMMENT         Clemson University Genomics Institute
                Clemson University
                100 Jordan Hall, Clemson University, Clemson, SC 29634
                Tel: 864 656 5737
                Fax: 864 656 4293
                Email: rdean@clemson.edu
                Seq primer: TAATACGACTCATATAGGG
                Class: BAC ends
                High quality sequence start: 58
                High quality sequence stop: 454.
FEATURES             Location/Qualifiers
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                     /strain="70-15"
                     /db_xref="taxon:148305"
                     /clone="mgxb0003F18f"
                     /tissue_type="protoplasts"
                     /lab_host="E. coli DH10B"
                     /clone_lib="CUGI Rice Blast BAC Library"
                     /note="Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII;
                     Rice blast is one of the most devastating fungal diseases
                     of rice world wide. It is a filamentous ascomycete with
                     a haploid genome (n=7) of approximately 40 Mbp. Rice
                     blast is an important model fungal pathogen for studying
                     numerous aspects of the fungal-host interaction. In
                     order to facilitate genome wide analysis, a BAC library
                     containing 9216 clones with an average insert size of 130
                     kbp was constructed. This library represents greater
```

than 25X genome coverage. High density colony filters
are available upon request."

genomic DNA flanking the left border of the pDs-Lox T-DNA
insert. PCR products were sequenced directly by using the
p745 primer 5' AACGTCCGCAATGTGTTATTAAGTTGTC 3'."

ORIGIN

Query Match    47.8%;  Score 351.8;  DB 11;  Length 839;
Best Local Similarity  99.4%;  Pred. No. 6e-99;
Matches 353;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy  379 AGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 438
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  163 ATTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 222

Qy  439 ATCGTGCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 498
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  223 ATCGTGCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 282

Qy  499 TGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTTCGCCGACAGTGGTCCCAAAGATGGA 558
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  283 TGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTTCGCCGACAGTGGTCCCAAAGATGGA 342

Qy  559 CCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 618
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  343 CCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 402

Qy  619 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG 678
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  403 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG 462

Qy  679 CAAGACCCTCCTCTATATAAGGAAGTTCATTTGGAGGAGGACACGCTGGA 733
        |||||||||||||||||||||||||||||||||||||||||||||
Db  463 CAAGACCCTCCTCTATATAAGGAAGTTCATTTGGAGGAGGACACGCTGAA 517
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ORIGIN

Query Match    46.8%;  Score 344.4;  DB 13;  Length 869;
Best Local Similarity  99.7%;  Pred. No. 1.3e-96;
Matches 345;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Qy  379 AGTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 438
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  113 ATTGAGACTTTCAACAAAGGGTAATATCGGGAAACCTCCTCGGATTCCATTGCCCAGCT 172

Qy  439 ATCGTGCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 498
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  173 ATCGTGCACTTCATCAAAAGGACAGTAGAAAAGGAAGGTGGCACCTACAAATGCCATCAT 232

Qy  499 TGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTTCGCCGACAGTGGTCCCAAAGATGGA 558
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  233 TGCGATAAAGGAAAAGGCTATCGTTCAAGATGCCTTCGCCGACAGTGGTCCCAAAGATGGA 292

Qy  559 CCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 618
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  293 CCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAA 352

Qy  619 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG 678
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  353 GTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCG 412

Qy  679 CAAGACCCTCCTCTATATAAGGAAGTTCATTTGGAGGAGGA 724
        |||||||||||||||||||||||||||||||||||||||||
Db  413 CAAGACCCTCCTCTATATAAGGAAGTTCATTTGGAGGAGGA 458
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Search completed: June  5, 2006, 07:59:05
Job time : 4661 secs

RESULT 15
LOCUS       CW799882             869 bp    DNA     linear   GSS 23-NOV-2004
DEFINITION  WiscDsLox391F04 Arabidopsis thaliana T-DNA insertion flanking
            sequences Arabidopsis thaliana genomic, genomic survey sequence.
ACCESSION   CW799882
VERSION     CW799882.1  GI:55997710
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 869)
  AUTHORS   Woody,S.T., Monson,S.S., Jester,P.J., Austin-Phillips,S.,
            Amasino,R.M., Sussman,M.R. and Krysan,P.J.
  TITLE     A New Community Resource for Knocking-Out Small Genes and
            Tandemly-Duplicated Gene Families and for Mosaic Analysis in
            Arabidopsis
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Woody ST
            Biotechnology Center
            University of Wisconsin-Madison
            425 Henry Mall, Madison, WI 53706, USA
            Tel: (608) 262-4640
            Email: swoody@facstaff.wisc.edu
            Class: TAIL-PCR.
FEATURES             Location/Qualifiers
     source          1..869
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                     /cultivar="Col-0 ecotype"
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                     /tissue_type="seeds produced by primary (Basta-resistant)
                     transformants"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion flanking
                     sequences"
                     /note="Vector: pDS-Lox; Sequence generated in the course
                     of an Arabidopsis T-DNA tagging program. TAIL-PCR was used
                     to generate sequencing templates that represent A.t.